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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                    on:
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198.605 Million cell updates/sec
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1325
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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               US-09-140-804-2
US-09-136-536-3
US-09-138-536-10
US-09-336-536-11
US-09-336-536-11
US-09-336-536-11
US-09-336-536-12
US-09-346-3911-2
US-08-463-911-7
US-09-140-804-3
US-09-140-804-3
US-09-136-536-12
US-09-136-536-13
US-09-136-536-13
US-09-136-536-13
US-09-336-536-22
US-08-463-911-4
US-09-336-536-13
US-09-346-20
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US-09-140-804-5
US-09-140-804-5
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13, Appli
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9, Appli
; Sequence 3, Application US/09336536
; Patent No. 6406884
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US-09-140-804-2
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219.5	219.5	219.5	221	223	223	224	228	228	229.5	229.5	229.5	240	243.5	251.5	257.5	266.5	276
16.6	16.6	16.6	16.7	16.8	16.8	16.9	17.2	17.2	17.3	17.3	17.3	18.1	18.4	19.0	19.4	20.1	20.8
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ALIGNMENTS

: Patent No. 6197930	
INI	ON:
; APPLICANT: Sheppard,	ard, Paul O.
; APPLICANT: Humes, Jacqueline ; TITLE OF INVENTION: ADTROCYTE	M.
	97-49
	APPLICATION NUMBER: US/09/140,804
: EARLIER APPLICAT	ADDITION NUMBER 60/05/ 003
FILING	DATE: 1997-08-26
OF SEQ	
; SEO ID NO 2	
NGTH:	
; TYPE: PRT	
; ORGANISM: Homo s US-09-140-804-2	sapiens
Query Match Best Local Similarity	100.0%; Score 1325; DB 4; Length 243; rity 100.0%; Pred. No. 9 5e-114.
nes 243;	vative 0; Mismatc
Qy 1 MRPLLY	MRPLLVLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG 60
Db 1 MRPLLV	
Qy 61 APGEKO	APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD 120
Db 61 APGEKG	
Qy 121 APLPED	APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ 180
Db 121 APLPED	
Qy 181 FFGGWP	FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP 240
Db 181 FFGGWP	
Qy 241 VFA 243	
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RESULT 2 US-09-336-536-3	
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US-09-188-930-295
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; TYPE: PRT
; ORGANISM: Homo s
US-09-336-536-3
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US-09-188-930-295
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CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 295
LENGTH: 243
                                                                                                       Query Match
Best Local Similarity
                                                                                                Matches
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                                                                                                                                                                                                                                                                                 APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
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TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATEENTIN Ver. 2.0
SEQ ID NO 3
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APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                           MRPLLVLLLIGIAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
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                                                                                            Conservative
                                                                                                     95.9%;
95.1%;
                                                                                   Score 1271; DB 4; Length 243;
Pred. No. 8.2e-109;
5; Mismatches 7; Indels
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; SOFTWARE: PatentIn Ver. 2
; SEQ ID NO 10
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-336-536-10
Sequence 4, Application US/09336536
Patent No. 6406884
GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: BOSSONE, S.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7983-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
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APPLICANT: McKay, C.
APPLICANT: McKay, C.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
COUNTRING OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                           241 VFA 243
                                                                                                                                                                                                                                                                                                                                                           181 YFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
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28; Conservative
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93.8%;
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Pred. No. 1.3e-
6; Mismatches
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APPLICANT: Heiby, K.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
ITILE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 228
TYPE: PRT
ORGANISM: Mus musculus
RESULT 7
US-09-336-536-7
; Sequence 7, Application US/09336536
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US-09-336-536-11
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                                                                                                                                                                                                                                                                                                                                                              Matches
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Patent No. 6406884
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Best Local Similarity 100.0%; Pred. No. 1.8e-107;

Matches 228; Conservative 0; Mismatches 0;
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Best Local Similarity
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 4
LENGTH: 228
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 94.7%;
                                                                                           181
                                                                                                                         196
                                                                                                                                                                    136 YDAVTGKFTCQVPGVYYFAVHATVYRASIQFDLYKNGBSIASFFQFFGGWPKPASLSGGA 195
                                                                                                                                                                                                             61 PRGEPGPRGEAGPMGAIGPAGECSVPPRSAFSAKRSESRVPPPADTPLPFDRVLLNEQGH 120
                                                                                                                                                                                                                                                                                                       16 SPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGRDGAPGAPGBKGBGGRPGLPG
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                                                                                                      MVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA 243
                                                                              MVRLEPEDQVMVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA 228
                                                                                                                                             YDPTTGKFTCOVPGVYYFAVHATVYRASLQPDLVKNGQSIASFFQYFGGWPKPASLSGGA
                                                                                                                                                                                                                                                                                SPPLDDNKIPSLCPGQPGLPGTPGHHGSQGLPGRDGRDGAPGAPGEKGEGGRPGLPG
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                                                                                                                                                                                                                                                                                                                                                    Score 1200; DB 4;
Pred. No. 2.4e-102;
5; Mismatches 7;
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APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: McKay, C.
APPLICANT: McKay, C.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THE REFERENCE: 7853-144
CURRENT APPLICATION UNUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
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US-09-336-536-14
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; ORGANISM: Homo sapiens
US-09-336-536-7
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APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 14
                                                                                                                                                            Matches 121;
                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/09336536
Patent No. 6406884
                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
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Best Local Similarity
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                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Mus
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                     225 STFSGFLV 232
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 121
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STFSGFLV 128
                                                                                                AFSAKRSESRVPPPADTPLPFDRVLLNEQGHYDFTTGKFTCQVPGVYYFAVHATVYRASL
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100.0%; Fr.
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100.0%; Pred. No. 1.2e-54;
cive 0; Mismatches 0;
                                                                                                                                                       Score 650; DB 4;
Pred. No. 2.3e-52;
4; Mismatches 3
                                                                                                                                                                                Length 128;
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RESULT 9 US-08-463-911-2

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RESULT 10
US-09-140-804-8
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Sequence 8, Application US/09140804
Patent No. 6197930
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIFOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617) 861-62
TELEPAX: (617) 861-9540
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI95-05
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA
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APPLICANT: Lodish, Harvey F.

TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED

TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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Massachusetts
                                                                                                                                                                                                                                                                                  FDLVKNGESIASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQV-GVGDYIGIYASIKTD
                                                                                                                                                                                                                                                                                                                                          FSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYPAVHATVYRASLQ 165
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Two Militia Drive
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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40.6%; Pred. No. 3.4e-32;
ative 32; Mismatches 97
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US-09-118-408-3
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                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09118408A Patent No. 6265544 GEMERAL INFORMATION:
                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                               Best Local
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SOFTWARB: FastSEQ for Windows Version 3.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 1998-07-17
EARLIER APPLICATION NUMBER: 60/053,154
EARLIER FILING DATE: 1997-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS FILE REFERENCE: 97-30 CURRENT APPLICATION NUMBER: US/09/118,408A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local
                                                                                                                                                                                                                                                                         LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo
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      118
                         106 FSAKRSESRYPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQ 165
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                                                                                      55 RDGAPGAPGEKGEGGRPGLPGPRGDPGPRGEAGPAGP-----TGPAGECSVPPRSA 105
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                                                                                                                                                        1 MRPLLVLLLL-GLAAGSPPLDDNKIPSLCPGHPG----LPGTPGHHGSQGLPGRDGRDG
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                                                                                                                                                                                                             Similarity
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FSV-GLETRVTVP-NVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSYHITVYMKDVK
                                                                                                                          LQALLFILILPSHAEDDVTTTEELAPALVPPPKGTCAGWMAGIPGHPGHNGTPGRDGRD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSLFKKDKAVLFTYDQYQE-KNVDQASGSVLLHLEVGDQVWLQVYGDGDHNGLYADNVND
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                                                                                                                                                                                               Conservative
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                                                             -GTPGEKGEKGDAGLLGPKGETGDVGMTGAEGPRGFPQTPGRKGEPGRAAYMYRSA
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                                                                                                                                                                                          Score 428.5; DB 4
Pred. No. 9.7e-32;
2; Mismatches 93
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Pred. No. 9.7e-32;
32; Mismatches 93;
                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                       Length 247;
                                                                                                                                                                                          Indels
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US-08-463-911-7

// Sequence 7, Application US/08463911

- Patent No. 5869330
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SOFTWARE: FASTSEQ for Windows Version 3.0; SEQ ID NO 3; LENGTH: 247
TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-506-855-3
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Best Local Similarity
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APPLICANT: Lasser, Gerald W.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND
TITLE OF INVENTION: IMMUNE FUNCTION
FILE REFERENCE: 99-12
                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                             APPLICANT: Scherer, Philipp E.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
                                                                                                                                NUMBER OF SEQUENCES:
OMPUTER READABLE FORM
                                COUNTRY:
                                                                              STREET:
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                                              Lexington
: Massachusetts
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                                                                                Two Militia Drive
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Query Match
Best Local Similarity
Matches 106; Conserva
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RESULT 14
US-09-140-804-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                           214 YIGIYASIKTDSTFSGFLVYSD 235
                                                                                                                  163 HITVYMKDVKVSLFKKDKAMLFTYDQYQENNVDQA--SGSVLLHLEVGDQVWLQVYGEGE
                                                                                                                                                156 HATTYYRASLQFDLVKNGES-IASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQV-GVGD 213
                                                                                                                                                                               105 GEGAYVYRSAFSV-GLETYVTIP-NMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAY 162
                                                            221 RNGLYADNDNDSTFTGFLLYHD 242
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                                                                                                                                                                                                                                               51 GAPGRÖCKD-----GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP 104
                                                                                                                                                                                                                                                                   45 GLPGRDGRDGAPGAPGAPGEKGEGGRPGLPGPRGD-----PGPRGEAGPAGPTGPA 95
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Pred. No. 2.5e-31;
                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                         PGHDQETTTQGPGVLLPLPKGACTGWMAGIPGHPGHN 50
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 244;
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NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Wir
SEQ ID NO 3
LENGTH: 244
                                                                                                                                                                                                                                                                 APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILLE REFERENCE: 97-49
CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09140804
Patent No. 6197930
                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                            for Windows Version 3.0
32.0%; Score 424; DB 4; Length 244; 40.5%; Pred. No. 2.5e-31; tive 26; Mismatches 72; Indels
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Conservative

58;

Gaps

10;

40.5%;

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GENERAL INFORMATION:

APPLICANT: Leiby, K.

APPLICANT: McKay, C.

APPLICANT: Bossone, S.

TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

FILE REFERENCE: 7853-144

CURRENT APPLICATION NUMBER: US/09/336,536

CURRENT FILING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 75

SOFTWARE: Patentin Ver. 2.0

ENOTH: 244

TYEB: PRT
ORGANISM: Homo sapiens
Search completed: June 20, Job time : 37 secs
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US-09-336-536-20
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                   Matches 106;
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                                                            221 RNGLYADNDNDSTFTGFLLYHD 242
                                                                                          214 YIGIYASIKTDSTFSGFLVYSD 235
                                                                                                                    163 HITVYMKDVKVSLFKKDKAMLFTYDQYQENNVDQA--SGSVLLHLEVGDQVMLQVYGEGE 220
                                                                                                                                           156 HATVYRASLQFDLVKNGES-IASFFQFFGGWPKDASLSGGAMVRLBFEDQVWVQV-GVGD 213
                                                                                                                                                                                    96 GECSVPPRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105
                                                                                                                                                                                                                                                   51 GAPGRDGRD-----GTPGEKGEKGDPGLIGPKGDIGETGVPGAEGPRGFPGIQGRKGEP 104
                                                                                                                                                                                                                                                                       45 GLPGRDGRDGAPGAPGAPGEKGEGGRPGLPGPRGD-----PGPRGEAGPAGPTGPA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 HATVYRASLQFDLVKNGES-IASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQV-GVGD 213
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                                                                                                                                                                                                                                                                                                                                                      6 VLLLLGLAAGSPPLDDNKIPSLCPGH------PG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 GECSVPPRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYPAV 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLLLIGLAAGSPPLDDNKIPSLCPGH-----PG----
                                                                                                                                                                                                                                                                                                                                                                                      32.0%; Score 424; DB 4; Length 244; ilarity 40.5%; Pred. No. 2.5e-31; Conservative 26; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                   ------PGHDQETTTQGPGVLLPLPKGACTGWMAGIPGHPGHN 50
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

AUTHORS	REFERENCE	SOURCE ORGANISM	RESULT 1 AX464228 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	
Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E., Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Waranahe, C. K.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1	human. Homo sapiens	AX464228 1377 bp DNA linear PAT 16-JUL-2002 Sequence 361 from Patent WO0140466. AX464228 AX464228.1 GI:21899130	

Pred. No. is the number of results predicted by chance to have a

	. GTGGGTGCAGGTGGGTGGGTGACTACATTGGCATCTATGCCAGCATCAAGACAGAC	Оу 841
ō	- GCCCAAGCCTCGCTCTCGGGGGGGGGCCATGGTGAAGGCTGGAGGACCTAAGT 84	Db 781
ō	GCCCAAGCCAGCCTCGCTCTCGGGGGGGGGCCATGGTGAGGCTGGAGGCTGAGGAC	Оу 781
õ	GTTTGATCTGGTGAAGAATGGCGAATCCATTGCCTCTTCTTCCAGTTTTTCGGGGGGGTG 78	Db 721
õ		Qy 721
20	CCAGGTGCCTGGGGTCTACTACTTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCA 72	Qy 661 Db 661
ő	CGACCGC	Db 601
ö	CGAC	Qy 601
0 0	CTTCAGCGCCAAGCGCTCCGAGAGCCGGTGCCTCCGCCGTCTGACGCACCCTTGCCCCTT 6	Qy 541 Db 541
ō	GGCGGACCCGCGGGCCCACCGGGCCTGCCGGGGAGTGCTCCGCTCCGCGATCCGC 54	Db 481
0		Qy 481
5 5	AGGCGAGGGCGGAAGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGA 48	N t
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š	CTTGCCCGGGCCGCGATGGCCGCGACGGCCGCGACGGCGCCCCGGGGCTCCCGGGAGAGAAA 42	Qy 361
	CAGCCTCTGCCCGGGCACCCCGGCCTTCCAGGCACGCCGGCCATGGCAGCAACGAGG 36	Db 301
60	CAGCCTCTGCCCGGGGCACCCCGGGCCTTCCAGGCACGCCGGGGCCACCATGGCAGGC 36	Фу 301
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6	GGGACTGCGAGAGGACCCCGGCGTCCCGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCT 24	1
	CCACTCCT 2	Оу 181
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	CCAACTGGAGGGTCCGGAGTAGCGAGCGCCCCGAACGAGGCCATCGGGAAGCCGAGCCGA	12
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20	TGGGGTGACGGCAGGGGGGGGGGCCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCA 1	0у 61
0 0	GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGAC 6	Qy 1 Db 1
0;	100.0%; Score 1377; DB 6; Length 1377; Similarity 100.0%; Pred. No. 1.3e-227; 77; Conservative 0; Mismatches 0; Indels 0; Gaps	Query Match Best Local : Matches 137
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ng	ood, W.L. and Zhang, Z. ecreted and transmembrane polypeptides and nucleic acids encodi acet. Wo 0140466 2 25 07 TWO 2001	TITLE S

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1370 bp mRNA linear PRI 16-MAY-2002 Homo sapiens, Clq and tumor necrosis factor related protein 5, clone MGC:32938 IMAGE:5278184, mRNA, complete cds. BC029485 BC029485.1 GI:20810468

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1370) Strausberg,R.

REFERENCE AUTHORS TITLE JOURNAL

Direct Submission
Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Genetics, National Cancer Collection, MD 20892-2590, National Cancer Drive, Room 11A03, Bethesda, MD 20892-2590, National Cancer Cancer Can

REMARK COMMENT

NII-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Sh
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Gen
Center, Stanford University School of Medicine, Stanford, CA
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and My CA 94305 Shiraki

Contact: (Di Dickson, M., R. M. A., and Myers,

Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.c. Series: IRAK Plate: 48 Row: h Column: 14 This clone was selected for full length sequencing because it information can be found http://image.llnl.gov

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                                                   Sheppard, P.O. and Humes, J.M.
Direct Submission
Submitted (20-DEC-2000) Bioinformatics,
Bastlake Ave. Bast, Seattle, WA 98102,
                                                                                                                                                         Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1337)
                                                                                                                                                                                                                                                    1337 bp mRNA
Homo sapiens complement-clq tumor necrosis
(CTRP5) mRNA, complete cds.
AF329841
                                                                                                                                Sheppard, P.O. and Humes, J.M. Homo sapiens complement-clq
                                                                                                                                                                                                                                         AF329841.1 GI:13274527
                                                                                                                    Unpublished
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                         Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                  tumor
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Conservative
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ASIKTDSTFSGFLVYSDMHSSPVFA"
ASIATO C 459 g 226 t
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/map="11q23.3"
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/product="complement-c1q tumor
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/db_xref="GI:13274528"
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1 (bases 1 to 134)

Sheppard, P.O. and Humes, J.M.
Sheppard, P.O. and Humes, J.M.
Adipocyte specific protein homologs

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Pred. No. 3.5e-218;
0; Mismatches 3;
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Matches 1065; Conse	1180 AGGAGTGTGCTGTGCTAGGTATGTAAGTCCCCCAGTTGCTCTGGTCCAGGAGCCCACGG 1239
ORIGIN Query Match Rest Local Similarit	1120 GGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCAG 1179
polyA signal polyA site	1060 TGACTAGGGAGGTGGGGTAGAGCACTCTCCGTCCTGCTGCTGCAAGGAATGGGAACAGT 1119
R G	1000 AGGGTGTGAGGCTGACCAGGTCATCCAGGAGGGTTGGCCCCCTGGAATATTGTGAA 1059
	940 CTCCCCAGTCTTTGCTTAGTGCCCACTGCAAAGTGAGCTCATGCTCTCACTCCTAGAAAG 999
gene //	880 TGCCAGCATCAAGACAGCACCTTCTCCGGATTTCTGGTGTACTCCGACTGGCACAG 939
	820 GCTGGAGGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGG
Source	760 CTTCCAGTTTTTCGGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGGGGG
Herin-Chainformation information at http://	700 CGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGAATCGATTGCCTCTTT 759
sequenced sequencing (DKFZp586B the RZPD)	640 CGTCACCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTACTTCGCCGTCCATGCCAC 699
COMMENT Clone from Research C	580 GTCTGACGCACCCTTGCCCTTCGACCGCGTGCTGGTGAACGAGGAGGAGGACATTACGACGC 639
	520 CTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTCCGAGAGCCGGGTGCCTCCGCC 579
M Hom Euk	460 GGACCCCGGGCCGCGAGGAGAGGGGGGGGGGGGGGGGCCGACCCGGGGCCTGCCGGGGAGTG 519
SO ION	400 GCCCGGGGGCTCCCGGGAGAGAAAGGCCGAGGGCGGGAGGCCGGGAACTCCCAAGG 459
	340 GGGCCACCATGGCAGCCAGGGCTTGCCGGGCCGCGATGGCCGCGACGGCCGCGACGGCGC 399
Oy 1360 AAAAAAA 	PRO ACTGGACGACAACAAGATCCCCAGCCTCTGCCCGGGGGCACCCCGGGCCTTCCAGGCACGCC 339
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1240	160 GCCATCGGGGAGCCGGGAGGGGGGAGAGGACCCCCGGCGTCCGGGCTCCCGGTGC 219
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/product="hypothetical protein"
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WPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSPVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                om S. Wiemann, Molecular Genome Analysis, German Cancer Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; by MediGenomix (Martinsried/Germany) within the CDNA og consortium of the German Genome Project. This clone 180621) is available at the RZPD in Berlin. Please contact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organisme"Homo sapiens"
/db_xref="taxon:9606"
/db_axef="taxon:9606"
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/tissue_type="uterus"
/clome_Tib="586 (synonym: hute1). Vector pSport1; host DH10B; sites Not1 + Sall/MluI"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ressourcenzentrum, Heubnerweg 6, 14059
arlottenburg, GERMANY; Email: clone@rzpd.de Further
on about the clone and the sequencing project is ava
//www.mips.biochem.mpg.de/proj/cDNA/.
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Score 1064.4; DB 9;
Pred. No. 9.2e-174;
0; Mismatches 1;
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L Published Only in Database (2002)

E (bases 1 to 191362)

B Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Pujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission

L Direct Submission
L Submitted (12-MAR-2001) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-Chou, Tsurumi. ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9171, Fax:81-45-503-9170.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yarai@ncc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phone: 81-3-3542-2511 ex 4752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    zip: 104-0045
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Mammalia; Eutheria;
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                                       Submitted (24-NOV-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Overlapping Clones: pD71A4, P038G8
Cytogenetic Position: 21q22.1, region:D21S226-AML STS Markers (ePCR): stSG53747, SHGC-16045, D11S2450, SHGC-7143,
                                                                                                                                                     Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 219,574 genomic DNA of 11q
Published Only in Database (2002)
2 (bases 1 to 219574)
Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
  stSG31054, sts-X57110, WI-8978, GDB:198117, stSG29284, SHGC-130657, D1151941E, WI-14589, stSG60191, stSG50535, A002048, stSG26946,
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National Cancer Center Research Institute
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                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (29-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-903-911, Fax:81-45-903-9170) On Nov 3, 2000 this sequence version replaced gi:8117391.
                                                                                             preserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Homo-sapiens 182, 429 genomic DNA of 11q23
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HOMO sapiens DNA, clone:RP11-680A7.
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Consensus quality: 175597 bases at least Q40
Consensus quality: 178555 bases at least Q30
Consensus quality: 179768 bases at least Q20
Consensus quality: 179768 bases at least Q20
Insert size: 180429; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of
                                                                                                                                                                                                                                                        Quality coverage: 9.01x in Q20 bases; sum-of-contigs
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Contact: hattori@gsc.riken.go.jp
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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54357 contig of
69839 contig of
84048 contig of
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NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is
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119058 119157: gap of 100 bp
119158 128134: contig of 8977 bp in length
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84149 95177: contig of 11029 bp in length
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54458 69839: contig of 15382 bp in length
69840 69939: gap of 100 bp
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66 163580: contig of 3915 bp in
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53 165252: gap of 100 bp
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69 178408: contig of 2603 bp in
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/db_xref≈"taxon:9606"
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145887: gap of 100 bp
15319: contig of 7212 bp in length
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107763: contig of 12486 bp in length
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128235. 136903
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119158. .128134
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107864. .119057
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34149. .95177
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Pred. No. 5.8e-145;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 4220)

Kameya,S., Hawes,N.L., Chang,B., Heckenlively,J.R., Naggert,J.K. and Nishina,P.M.
                                                                                                                                                                                                                                                    Mfrp, a gene encoding a frizzled related protein, mouse retinal degeneration 6
Hum. Mol. Genet. 11 (16), 1879-1886 (2002)
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AP469650
Mus musculus membrane-type frizzled-related protein (complement-clq tumor necrosis factor-related protein mRNAs_complete cds.
                                                                                                                                                                         Kameya, S., Naggert, J.K. and Nishina, P.M. Direct Submission
                                                                                                                                                Submitted (17-JAN-2002) The Jackson Laboratory,
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                                                                                                      Harbor, ME 04609, USA
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/chromosome="9"
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1 (Mfrp) and
In (Clqtnf5)
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  TGCTGCTAAATGAGCAGGGCCATTACGACCCCACTACTGGCAAGTTCACCTGCCAAGTGC
                          TGCTGGTGAACGAGCAGGACATTACGACGCCGTCACCGGCAAGTTCACCTGCCAGGTGC
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52. .1806
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FSSPNYPDLYPPLSHCVMHIQVAAGQTIQLKIQALSIESMLTCLEDBLEIISBETGPL
LRVCGKTPPATLATNTSHLLRVSFVSDNDVEGSGFQAWYQALFDBLEIISBETGPL
LCLKRDSVCDGITECADGSDEAANCSAKTLGCGGNLTGLYGVESTENVEQHYPHQQLCT
WYIEVPUGYGIRLEFHNFSLEAQAECKFDYVEVYEASNLGTESFLGRFCGAEPPLNVV
SSMHQLAVIFKTDLGISSGGFLATYQAINTTESGCFWAEFCGSGYRDLQWMCDLWKD
CANDSNDNCSSHLSPQPDLTCEPVQVEMCLGLSYNTTAFPNIWVGLATQTEVTDILRG
YKSLTSLECYQTFQRFLCGLLVPRCTSLGTILPPCRSVCQAAEQQCQSSLALLGTPWP
ENCNRLPVAASLEACSQP"
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/db_xref="G1:22033768"
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/translation="mretLALLLIGILVSGSPPLDDNKIPSLCPGOPGLPGTPGHHGSO
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RSAFSAKRSSEVPPPADTPLPFDRVLLNEQGHYDPTTGKFTCOVPGVYYFAVHATVY
RASLCJPDLVKMQSIASFGVPGAPULLNEQGHYDRTGIY
RASLCJPDLVKMQSIASFGVPGAPULLNEQGHYDRTGIY
ASIKTDSTFSGPLVYSDMHSSPVPA"
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SRLQAPWHAQRLRGLQPDCHFSWFCILLLSGLLLLLLLGLLVAVILAQLQATSLPRTTK
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/product="membrane-type frizzled-related
/protein ida="AAM89216.1"
/db_xref="GI:22023767"
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note="ClQTNF5"
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Pred. No. 2.3e-110;
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2 (bases 1 to 173038)

2 (bases 1 to 173038)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. & Fujiyama,A., Totoki,Y., Watanabe,H. & Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. & Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. & Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. & Fujiyama,A., Yada,Y., Yada,Y., Watanabe,H. & Fujiyama,A., Yada,Y., Y
                 Direct Submission
Submitted (05-JAN-2000) Masahira Hattori, The Institute of Physical
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DRAFT SEQUENCE,
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sapiens DNA, clone:RP11-680C5.
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chromosome 11 clone RP11-680C5 map 11q23, WORKING
CE, 28 unordered pieces.
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COMMENT

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NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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Japan (B-mail:hattori@gsc.riken.go.jp,
URL.http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
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                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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                  GCACTCTCCGTCCTGCTGGCAAGGAATGGGAACAGTGGCTGTCTGCGATCAGGTCTG 1140
                                                                      TCAT-CCAGGAGGGCTGGCCCCCC-TGGAATATTGTGAATGACTAGGGAGGTGGGGTAGA 1080
                                                                                                                         CACTGCAAAGTGAGCTCATGCTCTCACTCCTAGAAGGAGGGTGTGAGGCTGACAACCAGG
                                                                                                                                                                              CCTTCTCCGGATTTCTGGTGTACTCCGACTGGCACAGCTCCCCAGTCTTTTGCTTAGTGCC
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                                                                                                         CACTGCAAAGTGAGCTCATGCTCACTCCTAGAAGGAGGGTGTGAGGCTGACAACCTGG
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                                                       Conservative
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135391. .140229
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110123. .118116
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166758. .168307
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| 65317..166657
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163785. .165216
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|61844. .163684
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159918. .161743
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157374. .159817
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|50547. .153715
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147673. :150446
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143997. .147572
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132237. .135290
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118217. .126464
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Pred. No. 4e-110;
0; Mismatches
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TITLE
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                                                                            /Lissue_type="Mammary tumor. Metallothionien-TGF alpha
model. IO month old virgin mouse. Taken by biopsy."
/clone_lib="NCI_CGAP_Mam1"
/lab_host="DH10B"
/codon_start=1
/product="Unknown (protein
/protein_id="AAH25174.1"
/db_xref="GI:19263584"
                                                                note="Vector:
                                                                                                                                                           organism="Mus musculus"
db_xref="taxon:10090"
                                                                                                                              clone="MGC:36714 IMAGE:3978387"
                                                                                                                                               map="FVB/N"
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1141 GCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGAGCAGAGGAGTGTGCTGTGCTAGCAA
                                               Clone distribution: MGC clone distribution informat through the I.M.A.G.B. Consortium/LLID at: http://i Series: IRAK Plate: 61 Row: f Column: 24 This clone was selected for full length sequencing passed the following selection criteria: Hexamer fr
                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (DNA Sequencing by: Baylor College of Medicine Human
                                                                                                                                                                                                                     Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (05-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                                                                                                                                                                                                                                                                                                                                Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                        Sequencing Center
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                                                                                                                                  information can be found http://image.llnl.gov
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frequency
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Muzny, D.M.,
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CGTCCTGCTGCCAAGGAATGGGAACAGTGGCTGTCTGCGATCAGGTCTGGCAGCATG
                                             AGGAGGCTGGCCCCCCTGGAATATTGTGAATGACTAGGGAGGTGGGGGTAGAGCACTCTC
                                                                                                                                                CTGGATTTCTCGTCTATTCTGACTGGCACAGCTCCCCCAGTCTTCGCTTAAAACACAGTGA
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                                                                                                                  AAAGTGAGCTCATGCTCTCACTCCTAGAAGGAGGGTGTGAGGCTGACAACCAGGTCATCC
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Mus musculus, S
IMAGE:5355789,
BC023068
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                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Baylor College of Medicine Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (04-FEB-2002) National Institutes of Health, Mammalian Submitted (060), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
                                                                                                                                                                                                                                                                                                                                                                        Sequencing Center
Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                              Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1271)
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/db_xref="taxon:10090"
                         /note="Vector:
                                                                                               /clone="MGC:38635 IMAGE:5355789"
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Similar to DKFZP586B0621 j
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                                                                   C3(1)-Tag model.
d virgin mouse."
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Martin,
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AGGAGGGCTGGCCCCCTGGAATATTGTGAATGACTAGGGAGGTGGGGTAGAGCACTCTC 1088
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                                                  ACCCGGAGCTGGCACTTGCTCCTCAGTGGAGGGTGTGACACTAACCCGCGCAGCGCATAC
                                                                                AAAGTGAGCTCATGCTCCTCCTAGAAGGAGGGTGTGAGGCTGACAACCAGGTCATCC
                                                                                                            CTGGCGTCTACTACTTTGCTGTGCACGCCACTGTCTACCGGGCCAGCTTGCAGTTTGATC
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RASLQPDLVXNGQSIASFGQYPGGWYKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIY
RASIKTDSTFSGFLVYSDWHSSPVPA"
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Pred. No. 1.8e-109;
0; Mismatches 238;
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COMMENT	TITLE JOURNAL	TITLE JOURNAL REFERENCE AUTHORS	REFERENCE AUTHORS	VERSION KEYWORDS SOURCE ORGANISM	LOCUS DEFINITION	RESULT 13 AP001156	Db 1	82		φ γ	당 왕		<i>Q</i>	Db	92	Ф
ATKEN), Genomic Sciences Center (GSC Kitasato, Sagamihara, Kanagawa 228-8 sc.riken.go.jp, a.go.jp/, Tel:81-42-778-9923, quence version replaced gi:6997842.	Totoki,Y., Watanabe,H. and D) Masahira Hattori, The II	198,902 genomic DNA of 11q23 ly in DataBase (2000) to 198902) Ishii,K., Toyoda,A., Taylor,T.D.,	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 19802) Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yadda,T., Totoki,Y., Watanabe,H. and Sakaki Y.	AP001150 AP001156.2 GI:8118724 HTG; HTGS PHASE1; HTGS DRAFT. Homo sapiens DNA, clone:RP11-657A24. Homo sapiens			1236 CTTAATAAACCTAAAATCCTCAAAAAAAAAAAAAA 1271	1326 СТСААТАААССТААСААСССТСАТААЛААЛАЛАЛА 1361	CTCTAGGTCCCTGACTCCCATCTCCTGCTCCCAGGGCAGGCCTTTTTCTCAGAGGTCA	TCTCTGGATCCTCCCACCCCCTCCTGCTCCTGGGGCCGGCC	1209 - CCCCAGTIGGTCCAGGAGCCCAGGTGGGTGGTCTCTTCTTCCTGGTCCTCTGT 	GAGCAGTGGCTGGGTTTCTGCCCAGGACTTTA-GAATGCAGTAGGCTGGCAGCTGTGGGT	1149 GGGCAGTGGCTGGATTTCTGCCCAAGACCAGAGGAGTGTGCTGTGCTGGCTAGGCAAGTGTAAGT 1208	1014 GGTCCCACTGCTGGCAATGAATGGAGACAGGCTGTCTGAGGTCAAGACAGCGTG 1067	1089 CGTCCTGCTGGCAAGGAATGGGAACAGTGGCTGTCTGCGATCAGGTCTGGCAGCATG 1148	955 CAGGAGGGCTGGCCCCCTGGAATATTGTGAATGACTTAGGAAGAGAGGGGAG-CCACTTCC 1013

Center Flore name: RP11-657A24

Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of re Assembly program: Phrap; version 0.990329

Consensus quality: 171788 bases at least Q40

Consensus quality: 184443 bases at least Q20

Consensus quality: 191295 bases at least Q20

Insert size: 194802; sum-of-contigs

Quality coverage: 4.12x in Q20 bases; sum-of-cont Web site: http://hgp.gsc.riken.go.jp/ Contact: hattori@gsc.riken.go.jp ------ Project Information Center project name: HumDraft11 Center clone name: RP11-657A24 Center code: RIKEN Center: RIKEN Genomic Sciences Center (GSC)

reads

NOTE: This is a 'working draft' sequence. It currently consists of 42 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps

sum-of-contigs

밁 Ş 밁 S 밁 Ś 밁 S В S 밁 S 맑 δ 밁 Ś 밁 S 밁 S 밁 8 밁 Ś 밁 á В

δ

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194389
195759
197707 contig of 1949 bp in length
197808
198902 contig of 1095 bp in length
Sequence updated (26 May-2000).

* NOTE: This is a 'working draft' sequence. It currently
consists of 42 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 are unknown.
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                                                             58 5957: gap of 100 bp is 66804: contig of 7247 bp is 66804: gap of 100 bp is 66904: gap of 100 bp is 73970: contig of 7066 bp is 74070: gap of 100 bp is 74070: gap of 6937 bp is 81107: contig of 69
                                    81107: gap of
87320: con
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      100 bp
8/320: contig of 6213 bp in length
120: gap of 100 bp
93250: contig of
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1 (Dases 1 to 173657)

1 (Dases 1 to 173657)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Alsbrooks,S.L., Amaratunge,H.C., Blankenburg,K., Bonnin,D., Rarbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
                                                                                                                                                                                                                   AC112557 173657 bp
Rattus norvegicus clone CH230-904,
72 unordered pieces.
                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                     Rattus norvegicus
                                                                                                                                                                              AC112557
AC112557.2 GI:21735369
                                                                                   Rattus.
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31918. .41131
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41232. .49745
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Pred. No. 3.8e-96;
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TITLE
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37957: contig of 1453 b 38057: gap of unknown I 40293: contig of 2236 b 40393: gap of unknown I 41598: contig of 1305 b 41798: gap of unknown I 43155: contig of 1357 b 43255: gap of unknown I 45293: gap of unknown I 45293: contig of 1938 b 45293: gap of unknown I 47217: contig of 1924 b 47231: gap of unknown I 49331: gap of unknown I		1237: gap of unknown length 2820: gap of unknown length 2820: gap of unknown length 3984: contig of 1164 bp in 4088: gap of unknown length 5188: contig of 1074 bp in 6406: gap of unknown length 6306: contig of 1014 bp in 6406: gap of unknown length 7523: contig of 1117 bp in 7623: gap of unknown length 8631: contig of 1075 bp in 9906: gap of unknown length 11155: contig of 1249 bp in 11255: gap of unknown length 11255: gap of unknown length 11268: gap of unknown length 113604: gap of unknown length 13704: contig of 1133 bp in 14384: gap of unknown length 14931: contig of 1173 bp in 161844: gap of unknown length 161845: gap of unknown length 17958: gap of unknown length	. Gaps between , but the exact rd will be upda s it is availab ved. 1137: conti
738 ACTACTTCG	GGACTIGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGGAGGCGGGACCCGCGGGGGCCCGCGGGGCCGGGACCCCGCGGGGCCGGGACCCGCGGGGGCCAGGACCCGGGGGG	55643 57451: contig of 1809 bp in length 57452 57551: gap of unknown length 60852 609531: gap of unknown length 60852 609531: gap of unknown length 620952 62718: gap of unknown length 62719 63819 64976 65076: gap of unknown length 65077 65076: gap of unknown length 65077 67855: contig of 2158 bp in length 65076 67955: gap of unknown length 71314 71413: gap of unknown length 73660 73759: gap of unknown length 73760 73549: contig of 2246 bp in length 73550 73106: contig of 1308 bp in length 73550 73106: contig of 4345 bp in length 73550 73106: contig of 4345 bp in length 73551: contig of 4345 bp in length 73552 83651: gap of unknown length 83552 83651: gap of unknown length 83654 86153: gap of unknown length 86154 86153: gap of unknown length 96179 9201: contig of 2506 bp in length 92020 94877: contig of 2503 bp in length 92030 94877: contig of 2505 bp in length 92030 94877: contig of 2505 bp in length 94978 95947: contig of 2505 bp in length 96179 96201: contig of 2505 bp in length 96347 97047 98997: contig of 2505 bp in length 96348: contig of 2505 bp in length 96349 97047 98997: contig of 2505 bp in length 96341 97046: gap of unknown length 96341 97046: gap of unknown length 96341 97047 98997: contig of 2505 bp in length 97047 98997: contig of 2505 bp in length 97048: gap of unknown length 97049 98997: contig of 2505 bp in length 97049 98997: contig of 2505 bp in length 97040 97040: gap of unknown length 97040: gap of unknown length 97047 970	51205: contig of 1874 51305: gap of unknown 53117: contig of 1812 53217: gap of unknown 55542: contig of 2325 55642: gap of unknown 55640: gap of unknown 56640: gap of un

 121 CAIGGNWSNCARGGNYTNCCNGGNWGNGAYGGNWGNGAYGGNWGNGAYGGNGCNCCNGGN 180 407 GCTCCGGGAGAGAAAGGCGAGGGCGGGAGGCCGGGAACTGCCGGGACCTCGAGGGGACCCC 466	\$ 8
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287 GACAACAAGATCCCCAGCCTCTGCCCGGGGCACCCCGGCCTTCCAGGCACGCAC	Ş
 22/ ATGAGGICACTICCTGCTGCTGCTGCTGGGCTGGGCGGGCGGGTCGGCCCCACTGGAC 286	₽ \$
y to	Query Best Match
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I (bases 1 to 729) HORS Sheppard,P.O. and Humes,J.M. LE Adipocyte-specific protein homologs RNAL Patent: US 6197930-A 10 06-MAR-2001, RES Location/Qualifiers source 1. 729 /organism="unknown"	REFERENCE AUTHORS TITLE JOURNAL FEATURES sourc
MSIN	SOURCE ORGANISM
15 95 AR138195 729 bp DNA linear PAT 16-JUN-2001 TION Sequence 10 from patent US 6197930. N AR138195.1 GI:14479704 DS DS	RESULT 15 AR138195 LOCUS DEFINITION ACCESSION VERSION KEYWORDS
 44646 CTACAATCC 44654	рь
1336 CTAAGAACC 1344	Ş
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44526 ATCCTGGCTCAGGACTCCAAGATGGGATGCTCCCTTAGTCCTGTGCCCCTCTAGGTC 44585	ఠ
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                    ATCAAGACAGACAGCACCTICTCCGGATTICTGGIGTACTCCGACTGGCACAGCTCCCCA 946
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Search completed: June 20, 2003, 08:11:46
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AAF44999 AAF44999 AAF45000 AAF45001 AAL39624 AAS76911 AAS62228 AAF44971

6066

ABL34830 AAZ61635

AAZ61745 AAC99678

AAF45009 AAF45007

Human secreted pro
DNA escoding novel
cDNA sequence #15
Human TANGO 253 OR
Human secreted pro
Human secreted pro
Human secreted pro
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Murine secreted pro
CDNA encoding rat
Skin cell cDNA, SE
Rat cDNA isolated
CDNA encoding rat
Skin cell cDNA, SE
Rat cDNA isolated
Human colon cancer
Murine secreted pr

AAC99568 ABL34720 AAH33447 AAF44973 AAF45038 AAF45039 AAF45039

715.4 715.4 715.4 692.8 691.2 691.2 691.2

AAF44994 AAF44995 AAF44996 AAF44972

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Result
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AAZ61633 AAS76910 AAF44991

Human signal pepti Rat TANGO 253 codi DNA encoding novel

CDNA encoding rat Skin cell cDNA, SE Rat cDNA isolated

ALIGNMENTS

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98US-0083500. 98US-0086414	98US-0070440.	98US-0109304.	99WO-US00106.			/"Lag= C	5	/*tag= b	ũ	/*tag= a	227958	Location/Qualifiers			PRO344; UNQ303; cancer; tumour; diagnosis; therapy;		clone encoding human PRO344, amplified in tumo	(first entry)			AAX87258 standard; cDNA; 1377 BP.	

cDNA clone encoding human PRO344, amplified in tumour cells. PRO344; UNQ303; cancer; tumour; diagnosis; therapy; human; ss

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Best Local Similarity 100.0%;
Matches 1377; Conservative 0
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P-PSDB; AAY06481.
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10-NOV-1998;
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 CTTCAGCGCCAAGCGCTCCGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCTTGCCCTT
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PRO protein; tumour necrosis factor family; TNF; cytokine; transmembrane protein; inflammation disorder; 88

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03-DEC-1997;
11-DEC-1997;
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                                                                                                                                                                                                                                                                                                                      Sequence 1377
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16-DEC-1998;
22-DEC-1998;
20-JUL-1999;
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                                                   The present sequence encodes a novel human polypeptide. The specification describes novel polypeptides designated PRO201, PRO292, PRO327, PRO1265, PRO344, PRO347, PRO347, PRO357, PRO7115, PRO1017, PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumourigenesis. The polypeptides are useful target for the identification of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies against these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth
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                                                                                                                                                                                                                                                                                                                                New anti-polypeptide antibody useful in the neoplastic cell growth and proliferation -
                                                                                                                                                                                                                                                                                               Claim 50;
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New human nucleic acids encoding secreted and transmembrane polypeptides which are designated as PRO polypeptides are described. The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources.
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Sequence 1377 BP; 251 A; 422 C; 472 G; 232 T; 0 other; Score 1377; DB 21; Pred. No. 1.7e-244; Mismatches 0, Indels Length 0; Gaps 0

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04-DEC-1999;
04-JAN-2000;
14-FEB-2000;
18-FEB-2000;
                                                                                                                                                   01-DEC-2000;
                                                                                                                                                                                                                       Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alph cartilage; ear; proliferation; glucose; free fatty acid; skeletal adipocyte; A-peptide; factor VIIA; gene therapy; ss.
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                                                                                                                                                                                                          Homo sapiens.
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99WO-U330095
99WO-U330091
99WO-U330991
99WO-U331243
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2000WO-US131705
2000WO-US14042
2000WO-US14941
2000WO-US15264
2000WO-US15264
2000WO-US132673
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Gerritsen Smith V, Baker KP, PI; 2001-408281/43. PSDB; AAU12352. ME, Goddard Stewart TA, Beresini M, Deforge L, Desnoyers L, Filvaroff E, ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z 2 Ξ

Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical

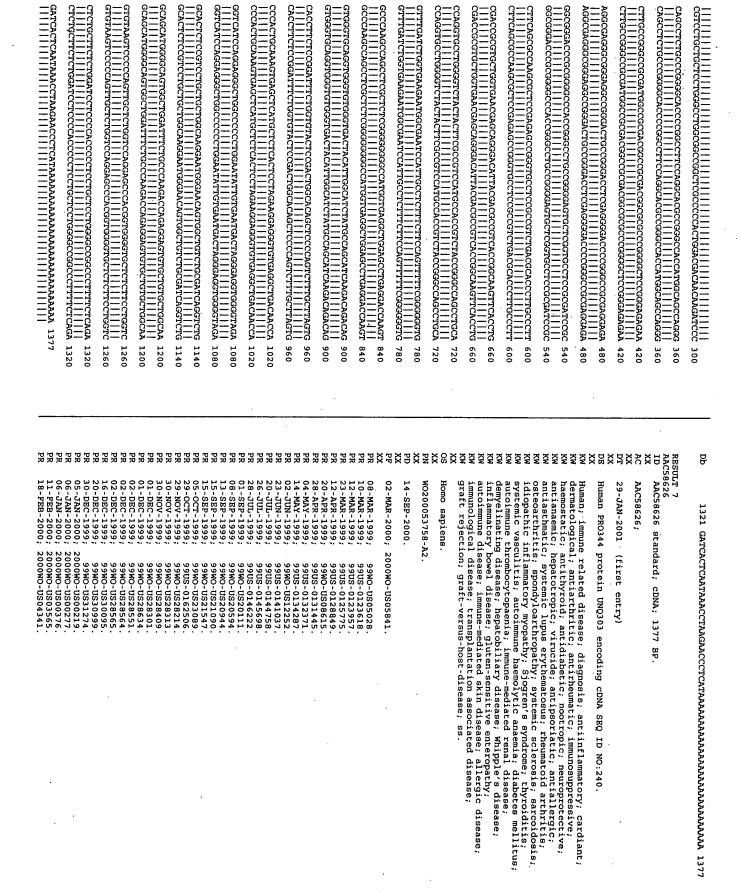
Claim 3; Fig 361; 813pp; English.

CC PRO polypeptides. The PRO polypeptides are useful to detect other CR PRO polypeptides, to link bioactive molecules to cells expressing CC PRO polypeptides, to modulate biological activities of cells expressing CC PRO polypeptides, and to detect the presence of mammalian lung, colon, CC polypeptides, and to detect the presence of mammalian lung, colon, CC polypeptide expression in a cell sample to that in a control sample. CC Some of the 275 sequences are also useful to stimulate the release of CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the CC proliferation or differentiation of chondrocytes, the proliferation or GC cartilage, the proliferation of immer ear utricular supporting cells or CC cartilage, the proliferation of immer ear utricular supporting cells or CC of T-lymphocytes, the release of a cytokine from peripheral blood CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of CC the PRO polypeptides may modulate glucose or free fatty acid uptake by CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify CC molecules involved in binding interactions. The polymuclocides encoding CC PRO polypeptides can be used to generate probes, antisense RNA/DNA, CC transgenic or knock out animals and can be used in gene therapy. AAS21244-AAS21518 encode for novel human secretory and transmembrane

Sequence 1377 BP; 251 A; 422 C; 472 G; 232 T; 0 other;

밁 δ 밁 ð B Ś 밁 Query Match Best Local S Matches 1377 121 121 181 181 61 61 _ μ. Similarity GGGACTGCGAGAGGACCCCGGGCGTCCGGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCT GACTAGTTCTCTTGGAGTCTGGGAGGAGGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGAC TGGGGTGACGGCAGGGGGGGGGCCTCGCCCGGGGAGAAGCGCCGGGGGCTCGAGCACCA TGGGGTGACGGCAGGGGGGGGGGCCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCA 100.0%; ilarity 100.0%; Conservative 0 ; Score 1377; DB 22; Pred. No. 1.7e-244; Mismatches 0, Indels Length 1377; 0 Gaps 120 240 180 180 120 60

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes sixty four human PRO proteins which be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful f treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1377 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumato arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
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Kabakoff RC,
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Query Match Best Local Similarity Matches 1324; Conser 40 CGCCAGGGA Y 40 CGCAGAGGA 11 CGAGAGGGA D 11 CGAGAGGGA T1 AGCGCGGGG T1 AGCGCGGGGG T1 AGCGCGGGGGG T1 AGCGCGGGGGG T1 AGCGCGGGGGG T1 AGCGCGGGGGG	metabolism by a polypeptide may cryopreservation to ischaemia and promoting lysis Sequence 1347 B	discovered, an cDNA allowed that allowed the adipocyte comp protein apM1. library. The vectors, culturare claimed, and are claimed.	This isolated polynucleot: protein zsig39 (AAW97984) nucleotides 243-962, 252-285-491, 285-49	1999-2 B; AAW 9 prot	26-AUG-1997; (ZYMO) ZYMOGE	04-MAR-1999. 26-AUG-1998;		mat_peptide	Key CDS	energy balance; nut Homo sapiens.	Adipocyte-spec
96.0%; Score 1322.2; DB 20; Length 1347; similarity 99.8%; Pred. No. 2e-234; t; Conservative 0; Mismatches 3; Indels 0; Gaps 0; ccgcnacgaaccaanccacgacraccaccaccaccaccaccaccaccaccaccaccacca	metabolism by administering a zsig39 polypeptide. The zsig39 polypeptide may also be used in organ preservation, for cryopreservation, for surgical pretreatment to prevent injury due to ischaemia and/or inflammation, and as an antimicrobial agent, promoting lysis or phagocytosis of infectious agents. Sequence 1347 BP; 235 A; 421 C; 465 G; 226 T; 0 other;	discovered, and the movel polypeptide encoded by the full-length cDNA allowed the identification of a homologue relationship with adipocyte complement related protein Acrp30 and adipocyte secreted protein apM1. A full-length clone was obtained from a lung tissue library. The zsig39 gene maps to the 11q23.3 region. Expression vectors, cultured cells and a method of producing zsig39 polypeptide are claimed, as well as probes and primers (useful in diagnostic	speci compris 185, 21 btide. by que cised 1 of app	765/17. 1984. 1 - used to modulate fatty acid metabolism 111; 132pp; English.	997; 97US-0056983. ZYMOGENETICS INC.	98WO-US17724:	/*tag= c /note= "alternatively nucleotides 243-926"	/*tag= b /note= "alternatively nucleotides 198-242" 252926	Location/Qualifiers 198.929 /*tag= a 198.251	crition; antimicrobial; s	ific protein; zsig39; human; fatty acid metabolism;
B	5 B & B &	, p 6 p 4	}	D	g g 29	Qy Db	Qy Db	D Qy	D Qy	Qy Db	Db
	940 CICCCAGICTINGCICAGIGCCACTGCAAAGIGAGCTCATGCICTCACTAGAAGG					460 GGACCCCGGGCCGCGAGGAGAGGCGGGGACCCGCGGGGCCCACCGGGCCTGCCGGGGAGTG		340 GGGCCACCATGGCAGGCCAGGGCTTGCCGGGCCGGATGGCCGCGACGGCGACGGCGCGACGGCGCGACGGCGCGACGGCGCGACGGCGCGACGGCGCGACGGCGCGACGGCGCGAACGGCCGACGGCGACGGCGACGGCGACGGCGACGGCGACGGCGACGGCGAACGGCGACGA	280 ACTGGACGACAACAAGATCCCCAGGCCTCTGCCCGGGGCACCCCGGGCCTTCCAGGCACGCC	220 CAGCGCTATGAGGCCACTCCTCGTCCTGCTGCTGGGCCTGGCGGCCTGGCGGCCCGGCTCGCCCCC	131 GCCATCGGGGAGCCGGGAGGGGGGACTGCGAGAGGACCCCGGGCGTCCGGGGCTCCCGGTGC

Qy 54 CCAGGACTGGGGTGACGGCAGGGCAGGGGCCTGGCCGGGAAAGCGCGGGGGCTGG 113 Db 15 CCGGGACTGGGGTGACCGGCAGGGCAGGGGGCCTGGCCGGGAAAGCGCGGGGGCTGG 74 Qy 114 AGCACCACCAACTGGAGGGTCCGGAGTAGCGAGGCCCTGGCCGGAAAGCACGAGGGCCTTGGAGGGCCATCGGGGAGGCCCCAACTGGAAGGGTCCGGAGTAGCGAGGCCCCCGAAAGGAAGCACCATCGGGGAGCCC 173 Db 75 AGCACCACCAACTGGAGGGTCCCGGAGTAGCAGCGCCCCGAAAGGAAGCACCCTATGAGGCC 134 Qy 174 GGGAAGGGGGAACTGCGAAGAGAACCCCCGGAGCTCCCGGAGGCCCACCGCTATGAAGCC 233 Db 135 GGGAAGGGGGACTGCCAAACCAGAACCACCGCTATGAAGGC 194 Qy 234 CACTCCTCGTCCTGCTGCTCCTGGGCCTGGCGGCTCCCGGCTCCCACTGGACGACAACA 293	Sequence 1338 BP; Query Match Best Local Similarity Matches 1310; Conset	XX XX CC The present invention provides the protein and coding sequences of the CC human and murine secreted or transmembrane proteins TANGO 253, TANGO 257, CC TANGO 281 and INTERCEPT 258. These are useful in the treatment of CC coronary, pulmonary, olfactory, immunological, neurological, CC developmental and kidney disorders.	atherosclerosis, infection disorders, brain disorders sclerosis and asthma sclerosis and asthma		PA (MILL-) MILLENNIUM PHARM INC. XX PI Leiby KR, McKay C, Bossone S;	PF 19-JUN-2000; 2000WO-US168B3. XX PR 18-JUN-1999; 99US-0336536.	PN WO200078808-A1. XX PD 28-DEC-2000.	developmental developmental.	Human; mouse; secreted protein; TANGO253; INTERCEPT 258; coronary disorder; olfactory		AAP44970 ID AAP44970 standard; cDNA; 1338 BP. XX AC AAP44970.	Db 1331 AAAAAAA 1337	Db 1271 GGGCCGGCCCTTTTCTCAGAGATCACTCAATAAACCTAAGAACCCTCAAAAAAAA	Qy 1300 GGGGCCGGCCTTTTCTCAGAGATCACTCAATAAACCTAAGAACCCTCATAAAAAAAA
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AGSTCTGGCAGCATGGGCAGTGGCTGAATTCTGCCCAAGACCAAGAGGAGTGTGCTGTGCTTGTTGGCCAAGTGTAAGTCCCCCAGTTGGCTCTGTTCCTGGCCAAGACCAAGAGCACGAGGAGTGTGCTCTCTTTTTTGGCCAAGTTGTTCCCCAGTTGGTCCAGGAGCCCACGGTGGGGTGCTCTCTTTTTTGTTCAGAAGTCCTCCCAGTTGCTCCTTGTTCCAGGAGCCCACGTTGGGTGCTCTCTTTTTTTT	974 ACAACCTGGTCATCCAGGAGGGCTGGCCCCCTGGAATATTGTGAATGACTAGGGAGGTG 1033 1074 GGGTAGAGCACTCTCCGTCCTGCTGCTGGCAAGGAATATTGTGAATGACTAGGGAGGTG 1133	954 CTTAGTIGCCCACTIGCAAAGTGAGCTCATGCTCTCACTCCTAGAAGGAGGGTGTGAGGCTG 1013	894 CAGACAGCACCTTCTCCGGATTTCTGGTGTACTCCGACTGGCACAGCTCCCCAGTCTTTG 953	834 ACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTACATTGGCATCTATGCCAGCATCAAGA 893	774 GGGGTTGGCCCAAGCCAGCCTCGCTCTCGGGGGGGGCCATGGTGAGGCTGAGGCTGAGG 833	714 GCCTGCAGTTTGATCTGGTGAAGAATGGCGAATCCATTGCCTCTTTCCTTCC	654 TCACCTGCCAGGTGCCTGGGGTCTACTACTTCGCCGTCCATGCCACCGTCTACCGGGCCA 713	594 TGCCCTTCGACCGCGTGCTGGTGAACGAGCAGGAGCAGTACGACGCCGTCACCGGCAAGT 653	534 GATCCGCCTTCAGCGCCAAGCGCTCCGAGAGCCGGTGCCTCCGCCGTCTGACGCACCCT 593	474 GAGGAGAGGCGGGACCCGCGGGGCCCACCGGGCCTGCCGGGGAGTGCCTCCGCTCCGC 533	414 GAGAGAAAGGCGAGGGCGGGAGGCCGGGACCTCGAGGGGACCCCCGGGCCCGC 473	354 GCCAGGGCTTGCCGGGGCCGCGATGGCCGCGACGGCGCGCGC	294 AGATCCCCAGCCTCTGCCCGGGCACCCCGGCCTTCCAGGCACGCCGGGCCACCATGGCA 353	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences of the human and murine secreted or transmembrane proteins TANGO 253, TANGO 257, TRANGO 281 and INTERCEPT 258. These are useful in the treatment of coronary, pulmonary, olfactory, immunological, neurological, developmental and kidney disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acids for treating diseases and disorders, e.g. atherosclerosis, infection, autoimmune diseases, obesity, ear disorders, brain disorders, tumors, diabetes, arthritis, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1338 BP; 229 A; 422 C; 460 G; 227 T; 0 other;
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                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of human and murine secreted or transmembrane proteins TANGO 253, TANG TANGO 281 and INTERCEPT 258. These are useful in the treatment of coronary, pulmonary, olfactory, immunological, neurological, developmental and kidney disorders.
                                                                                                                                                                                                                                                                                                                                                           New nucleic acids for treating diseases and disorders, e.g. atherosclerosis, infection, autoimmune diseases, obesity, ear disorders, brain disorders, tumors, diabetes, arthritis, multiple sclerosis and asthma -
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secreted protein; TANGO253;
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protein related coding sequence SEQ ID NO: 107.

TANGO

TANGO

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713

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Query Match
Best Local Similarity
Matches 1309; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acids for treating diseases and disorders, e.g. atherosclerosis, infection, autoimmune diseases, obesity, ear disorders, brain disorders, tumors, diabetes, arthritis, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 273; 332pp; English.
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                                                                        Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281; INTERCEPT 258; coronary disorder; olfactory disorder; neurological disorder; pulmonary disorder; immunological disorder; developmental disorder; kidney disorder; ss.
WO200078808-A1
                                                                                                                                                                                                Human
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TANGO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                          GATCCGCCTTCAGCGCCAAGCGCTCCGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCT
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AAL39624 standard;

DNA;

3248 ΒP

secreted protein entry) DNA SEQ ID

No

RESULT 14
AAL39624
ID AAL39
AC Antiarteriosclerotic; cytostatic; HIV; antiallergic; antianaemic; antiasthmatic; cardiant; vasotropic; neuroprotective; nootropic; SECP; anticonvulsant; antiparkinsonian; cerebroprotective; antiinflammatory; immunosuppressive; human secreted protein; cell proliferative disorder; arteriosclerosis; cancer; autoimmune; inflammatory disorder; AIDS; allergy; anaemia; asthma; cardiovascular disease; developmental disorder; ischaemic heart disease; congestive heart failure; neurological disorder; renal tubular acidosis; hypothyroidism; Alzheimer's disease; dementia; parkinson's disease; epilepsy; stroke; knockin humanised animal; gene therapy; gene; ds.

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                                                                                                                                                                                                                                                                                                                                CC The invention relates to an isolated human secreted protein (SECP)
CC polypeptide from 63 fully defined protein sequences given in the
CC specification. The polypeptide is useful for the diagnosing/treating of a
CC disease with decreased/overexpression of SECP. Examples of disorders
CC associated with abnormal expression of SECP include a cell proliferative
CC disorder e.g. arteriosclerosis, cancers; autoimmune/inflammatory
CC congestive heart failure, ischaemic heart disease; developmental disorder
CC crapestive heart failure, ischaemic heart disease; developmental disorder
CC re.g. renal tubular acidosis, hypothyroidism, neurological disorder e.g.
CC The SECP polymucleotide and polypeptide are further useful for analysing
CC reating knockin humanised animals (pigs) or transgenic animals (mice or
CC rates) to model human disease, and for somatic or germline gene therapy,
CC and further for generating hybridisation probes useful in mapping the
CC represents the DNA of a human secreted protein of the invention.
                                                                                                                                                                                                                                                                        Query Match
Best Local Sim
Matches 1222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-NOV-2000;
21-NOV-2000;
08-DEC-2000;
18-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted proteins and polynucleotides for diagnosing, treating preventing disorders of cell proliferative, cardiovascular, developmental, neurological and autoimmune/inflammatory disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ding L,
Lu DAM,
                                                                                                                                                                                                                                                                                                                                Sequence
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P-PSDB; AAO21663.
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09-NOV-2000;
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                                                                                                                                                                                                                                                                                     Similarity
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ala M, '
GCTGCTCCTGGGCCTGGCGGCCCGGCTCGCCCCCACTGGACGACAACAAGATCCCCAGCCT
                                                   GCGAGAGÉACCCCGGCGTCCGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCCT
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la M, Thornton M, Elliott VS, Lu Y, Gietzen KJ, Burfo
Hafalia AJA, Tang YT, Bandman O, Warren BA, Honchell
Thangavelu K, Lee S, Xu Y, Yang J, Lal PG, Tran B;
Duggan BM, Sapperstein SK;
                                                                                                                                                              GACGGCAGGGCAGGGCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCAACT
                                                                                                                                                                                                                                      TTCTCTTGGAGTCTGGGAGGAAAGCCGGAGCCGGCAGGAACCAGGACTGGGGT
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; 2000US-249824P.
; 2000US-252824P.
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; 2000US-256448P.
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                                                                                                                                                                                                                                                                                    78.8%;
90.5%;
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Pred. No. 1.1e
0; Mismatches
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KJ, Burford N;
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                         TCAATAAACCTAAGAACCCTCATAAAAAAA 1356
                                                             TTCTCTGGATCCTCCCCACCCCCTCCTGCTCCTGGGGCCCGTTTTCTCAGAGATCAC
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CTGCCCGGGGCACCCCGGCCTTCCAGGCACGCCGGCCCACCATGGCAGCCAGGGCTTGCC

RESULT

AAS76911

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CN Note: The sequence data for this patent did not appear in the printed CC at the wiso.int/pub/sublished pct sequences.
                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                Matches 1042; Conservative
                                                                                                                                                                                                                                            Sequence 1082 BP; 193 A; 334 C; 353 G; 202 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID No 12715; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
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DB; ABG12724.
                     359 GGCTTGCCGGGCCGCGATGGCCGCGACGGCCGCGCGCCCCGGGGCTCCCGGAAGAG
                                                                                                   299 CCCAGCCTCTGCCCGGGCACCCCGGCCTTCCAGGCACGCCGGGCCAGCGATGGCAGCCAG 358
      19
GGCTTGCCGGGCCGATGGCCGACGGCGACGGCGCCCCGGGGCTCCGGGAAAAG
                                                                              CCCAGCCTCTGCCCGGGCACCCCGGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAG
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96.5%;
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Pred. No. 4.4e-161;
0; Mismatches 24; Indels 14;
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Db 102	Qу 130	Db 96	Оу 124		0у 118	80	Оу 112	7	Qу 107	Db 72	Оу 101	Db 66	Оу 95	Db 60		σ	Ωу 8:	Db 4	Оу 7	Db 4:	· Qy 7	Db 3	δλ .	Db 3	Qy 5	N	5 40	Db 1	0у 4	Db 1	Qy 41
1 GCCCTTTTCTCAAG	7 GCCCTTTCTCA	μ.	7	-	8	_	ω	81 TTGGGGGTAGAGCACTCTCCAGTCC	ผ	-	w	1 TAGTGCCC	6 TAGTGCCC	01 AGCACCTTCTCCGGATTTCTGGTGT	99 AGCACCTTCTCCGGATTTCTGGTGT	41 GTGTGGGTGCAGGTGGGTGTGGGTC	39 GIGTGGGTGCAGGTGGGTGTGGGTG	81. TGGCCCAAGCCAGCCTCGCTCTCGG	79 TGGCCCAAGCCAGCCTCGCTCTCGC	21 CAGTITGATCTGGTGAAGAATGGCC	9	61 TGCCAGGTGCCTGGGGTCTACTACT	59 TGCCAGGTGCCTGGGGTCTACTACT	01 TTCGACCGCGTGCTGGTGAACGAGC	99 TTCGACCGCGTGCTGGTGAACGAGC	41 GCCTTCAGCGCCAAGCGCTCCGAGZ	39 GCCTTCAGCGCCAAGCGCTCCGAG	81 GAGGCGGGACCCGCGGGGCCCACCC	79 GAGGCGGGACCCGCGGGGCCCACCC	.21 AAAGGCGAGGGCGGGAGGCCGGGAC	١
HGATCCACTCAATAAACCTAAGAACCCTCAAAAAAAAAAA	AATAAACCTAAGAACCCTCATAAAAA	CTCTCTTCCTGGTCCTCTGGCTTCTCTGGATCCTCCCACCCCCTCCTGCTCCTGGGGG	TEGATCCTCCCACCCCCTCCTGCT	GCTGTGGTGGGAAGTTGTAAGTCCCCCAGTTGCTTTGGTCCAGGAGCCCACGGTGGGGTG	CCAGTIGCICIGGTCCAGGAGCCCA		CAGTGGCTGGATTTCTGCCCAAGACC	TIGGGGTAGAGCACTCTCCAGTCCTGCTGCTGCAAGGAATGGGGAACAGTGGCTGTCT	стестестессаледалат-еедласа	GACAACCAGGTCATCCAAGGAGGGCTGGCCCCCCCTGGAATATTTGTGAATGACTAGGGAAG	CTGGCCCCCCTGGAATATTGTGAATG	CACTGCAAAAGTGAGCTCATGCTCTCAACTCCTAGAAGGAGGGTGTGAGGCT	TCATGCTCTC-ACTCCTAGAAGGAGG	AGCACCTTCTCCGGATTTCTGGTGTACTCCGACTGGCATCAGCTCCCCCAGTCTTTAGCT	TACTCCGACTGGCACAGCTCCCC	GTGTGGGTGCAGGTGGGTGAGTGACTACATTGGCATCTATGCCAGCATCAAGACAGAC	GACTACATTGGCATCTATGCCAGCAT	TGGCCCAAGCCTCGCCTCTCGGGGGGGGGCCATGGTGAGGCTGGAGCCTGAGGACCAA	GGGGGGCCATGGTGAGGCTGGAGCC	CAGTTTGATCTGGTGAAGAATGGCGAATCCATTTGCTCTTCCTGCCAGTTTTTCCGGGGGG	GAATCCATTGCCTCTTTCTTCCAGTT	TGCCAGGTGCCTGGGGTCTACTTCGCCGTCCATGCCACCGTCTACCGGGCCAG	TTCGCCGTCCATGCCACCGTCTACCG	TICGACCGCGTGCTGGTGAACGAGCAGGGACATTACGACGCCGTCACCGGCAAGTTCAC	CAGGGACATTACGACGCCGTCACCGG	CTTCAGCGCCAAGCGCTCCGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCTTGC	AGCCGGGTGCCTCCGCCGTCTGACGC	HAGGCGGGACCCGCGGGCCCACCGGGCCTGCCGGGGAGTGCTCCGCTGCCTCCCCCC	geeccrecceegagrecreerecc	AAAGGCGAGGCGGGAGGCCGGGACTTGCCGGGACCTCGAGGGGACCCCCGGGCCGCGAGGA	
AAAAAAAAA 1080	ААААААААА 1364	CCTGGGGCCG 1020	ccreeeecce 1306	960	12	90	AGAGGAGTGT 1187	84	GIGGCIGTCT 1127	ACTAGGGAGG 780	ACTAGGGAGG 1071	GIGIGAGGCT 720	GTGTGAGGCT 1012	GTCTTTAGCT 660	9	6	CAAGACAGAC 898	TGAGGACCAA 540	TGAGGACCAA 838	TTTCGGGGGG 480	TTTCGGGGGG 778	GGCCAGCCTG 420	GGCCAGCCTG 718	CAAGTTCACC 360	CAAGTTCACC 658	ACCCTTGCCC 300	ဂ္ဂ	TCCGCGATCC 240	TCCGCGATCC 538	GCCGCGAGGA 180	

Search completed: June 20, 2003, 06:55:51 Job time : 353 secs

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Minimum
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TYPE: DNA
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US-09-298-568-3	US-08-843-659-1	US-09-259-821A-1	US-08-690-473-1	US-08-406-030A-3	US-09-397-787-161	US-09-103-840A-2	US-09-103-840A-1	US-08-655-086-1	US-09-506-855-1	US-09-118-408-1	US-08-642-255-48	US-09-230-371A-16	US-08-757-669A-16	US-08-770-379-16	US-09-227-357-51	PCT-US96-01427-1	US-08-999-336-1
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ALIGNMENTS

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; LOCATION: (198)...(926)
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SEQ ID NO 1
LENGIH: 1347
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Best Local Similarity 99.8
Matches 1324; Conservative
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APPLICANT: Humes, Jacqueline M.
APPLICANT: Humes, Jacqueline M.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
CURRENT FAPPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER APPLICATION NUMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
COUNTAINED TO COMMENT OF THE PROPERTY OF THE PROP
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GGGCCACCATGGCAGCCAGGGCTTGCCGGGCCGCGATGGCCGCGACGGCCGCGACGGCGC
                                                                                                                                         ACTGGACGACAACAAGATCCCCAGCCTCTGCCCGGGGCACCCCGGCCTTCCAGGCACGCC
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; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leiby, K.
; APPLICANT: MCKAY, C.
; APPLICANT: BOSSONE, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND US!
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336,536
; CURRENT APPLICATION NUMBER: US/09/336,536
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1338
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-336-536-1
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Best Local Similarity
Matches 1310; Conserv
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GATCCGCCTTCAGCGCCAAGCGCTCCGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCT
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                                                                             TCACCTGCCAGGTGCCTGGGGTCTACTACTTCGCCGTCCATGCCACCGTCTACCGGGCCA
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Pred. No. 7.7e-252;
0; Mismatches 4;
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CURRENT APPLICATION NUMBER: US/09/336,536; CURRENT FILING DATE: 1999-06-18; NUMBER OF SEQ ID NOS: 75; SOFTWARE: PatentIn Ver. 2.0; SEQ ID NO 2; SEQ ID NO 2; LENGTH: 728; LENGTH: 728; TYPE: DNA; ORGANISM: Homo sapiens
US-09-336-536-2
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Patent No. 6406884
GEMERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND FILE REFERENCE: 7853-144
                                                                                                                                                         Query Match
Best Local Similarity
Matches 728; Conserv
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              CTGGCAAGTGTAAGTCCCCCAGTTGCTCTGGTCCAGGAGCCCACGGTGGGGTGCTCTCTT
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99.9%;
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Pred. No. 1.4e-135;
0; Mismatches 0;
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; SEQ ID NO 8
; LENGTH: 1263
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-336-536-8
                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND US:
FILE REFERENCE: 7853-144
CURRENT APPLICATION UMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
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Best Local Similarity 78.0%;
Matches 917; Conservative
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TGCTTCTGGGTCTGGTCAGGCTCTCCTCCTCGGACGACAACAAGATCCCCAGCCTGT
             TGCTCCTGGGCCTGGCCGGCCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCT 308
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                                                                                                 Score 692.8; DB 4;
Pred. No. 1.1e-130;
0; Mismatches 237;
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                                                                       CTTCTCTGGATCCTCCCCACCCCCCTCCTGCTCCTGGGGCCCGTTTTCTCAGAGATCA 1325
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GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated Fro
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT APPLICATION STREET CONTINUES CONTROL APPLICATION OF STREET CONTROL 
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; TYPE: DNA
; ORGANISM: Rat
US-09-188-930-218
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US-09-188-930-218
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Patent No. 61505
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Best Local Similarity
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                                                        GCCAGGTGCCTGGGGTCTACTACTTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGC
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Pred. No. 2.7e-113;
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APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Ski
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 78.9
Matches 738; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 30
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TYPE: DNA
ORGANISM: Rat
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                   TG-----CGAGAGGACCCCGGCGTCCCGGGTGCCAGCGCTATGAGGCCACTCC
  CCAGCCTCTGCCCGGGGCACCCCCGGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGG
                                                                                                          TTGCCCTGCTTCTGGGTCTGGCATCAGGCTCTCCTCTGGACGACAACAAGATCC
                                                                                                                          TOGTCCTGCTGCTCCTGGGCCTGGCGCCCGCGCTCGCCCCCACTGGACGACAACAAGATCC
                                                                                                                                                               AGACTACAAGAGAGGATCCTGGCGTCTGGGCCTCCTGGGTCATCACCATGAGGCCACTTC
                                                                                                                                                                                                                    GTCTGAGGAAGCCATTCAAAGCGAGCAGCTGGGAGAGCTGGGGAGCCGGGAAGGGCCTAC
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78.5%;
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                                                                                                                                                                                                                                                                                                                           Score 605; DB 3; Length 10
Pred. No. 4.3e-113;
0; Mismatches 196; Indels
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                                                                                                                                                                                                                                                                                                                                                       Length 1015;
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                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Leiby, K.

APPLICANT: McKay, C.

APPLICANT: Bossone, S.

TITLE OF INVENTION: SECRETED PROTEINS AND US:

FILE REFERENCE: 7853-144

CURRENT APPLICATION NUMBER: US/09/336,536

CURRENT APPLICATION NUMBER: US/09/336,536

CURRENT FILING DATE: 1999-06-18

NUMBER OF SEQ ID NOS: 75

SOFTMARE: Patentin Ver. 2.0

SEQ ID NO 9

LENGTH: 729

TYPE: DNA

ORGANISM: Mus musculus

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US-09-336-536-9
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                                                                                                      Query Match
Best Local Similarity
Matches 626; Conserv
                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/09336536 Patent No. 6406884
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GACAACAAGATCCCCAGCCTCTGCCCGGGGCACCCCGGGCCTTCCAGGCACGCCGGGCCAC 346
                                                                 GGCCCAAGCCAGCCTCGCTCTCGGGGGGGGCCATGGTGAGGCTGGAGGCCTGAGGACCAAG
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                                                   ATGAGGCCACTTCTTGCCCTTCTGCTTCTGGGTCTGGTCAGGCTCTCCTCCTCTGGAC
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                                                                                                         Conservative
                                                                                                                    41.0%;
85.9%;
                                                                                                       0;
                                                                                                       Score 564.2; DB 4;
Pred. No. 6.2e-105;
0; Mismatches 103;
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                                                        ; OTHER INFORMATION:
; OTHER INFORMATION:
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Best Loca
Matches
                                                                                                                                          SEQ ID NO 10
LENGTH: 729
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                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/09140804 Patent No. 6197930
                            Query Match
                                                                                                                                                                                                            APPLICANT: Sheppard, Paul O.
APPLICANT: Humes, Jacqueline M.
APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
FILE REFERENCE: 97-49
FILE REFERENCE: 97-49
CURRENT APPLICATION NUMBER: US/09/140,804
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: 60/056,983
                                                                                                                                                                    EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSEQ for Windows Vo
                                                                                                  FEATURE:
                                                                                                              ORGANISM: Artificial
                                                                                                                               TYPE: DNA
              Local Similarity
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                                                                    Degenerate nucleotide polypeptide of SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                            955
                                                                                                              Sequence
                                                                                                                                                                       Windows Version
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  164;
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 0
                                                 APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND US
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
UNUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 74
                                                                                                                                                                                                            US-09-336-536-74; Sequence 74, Application; Patent No. 6406884
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LENGTH: 601
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
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; ORGANISM: Rat
US-09-188-930-26
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US-09-188-930-26
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26, Application US/09188930A
Patent No. 6150502
GENERRAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000,1011c1
   Query Match
Best Local Similarity
Matches 250; Conserv
                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
LENGTH: 393
TYPE: DNA
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Best Local Similarity
Matches 365; Conserv
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09
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   Score 149.6; DB 3;
Pred. No. 8.6e-22;
0; Mismatches 104;
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Pred. No. 1.8e-43;
0; Mismatches 134;
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NAME/KEY:
LOCATION:
S-08-463-911-1
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Patent No. 5869330
                                                                                                                                  TELEFAX: (617) 861-954
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                REFERENCE/DOCKET NUMBER: WH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                           MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Scherer, Philipp B.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: A NOVEL SERUM P
TITLE OF INVENTION: EXCLUSIVELY IN
                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: M
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                                                                           TOPOLOGY:
                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                          CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                      LENGTH:
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N ADIPOCYTES
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Best Local
                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08463911 Patent No. 5869330
                                                                                                                                                                                                                                                                            APPLICANT:
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                          TITLE OF INVENTION:
SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                          STREET:
                                                                                                                      COUNTRY:
                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                      Lexington
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                                                                                                                                                                        Two Militia Drive
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                                                                                                                                                                                                                                                                            Lodish,
                                                                                                                        USA
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                                                                                                                                                                                        Hamilton, Brook,
                                                                                                                                                                                                                                          , Philipp B.

Harvey F.

A NOVEL SERUM PROTEIN PRODUCED
EXCLUSIVELY IN ADIPOCYTES
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Pred. No. 7.3e-10;
D; Mismatches 279;
                                                                                                                                                                                            Smith
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                  Version #1.30
                                                                                                                                                                                            & Reynolds,
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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Best Local :
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (gen
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NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
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Pred. No. 3.6e-08;
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; TYPE: DNA; ORGANISM: Homo sapiens US-09-140-804-9
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CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION UNMBER: 60/056,983
EARLIER FILING DATE: 1997-08-26
NUMBER OF SEQ ID NOS: 47
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
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Best Local Similarity
Matches 316; Conserv
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Sequence 23, Application US/09118408A Patent No. 6265544 GENERAL INFORMATION:
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APPLICANT: Humes, Jacqueline M.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOWOLOGS
FILE REFERENCE: 97-49
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Pred. No. 4.4e-08;
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LENGTH: 843
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Best Local
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OTHER INFORMATION: Each N
-09-118-408-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/118,408A CURRENT FILING DATE: 1998-07-17 EARLIER APPLICATION NUMBER: 60/053,154 EARLIER FILING DATE: 1997-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN
FILE REFERENCE: 97-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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NAME/KEY: variation
(1)...(843)
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OTHER INFORMATION: Degenerate
OTHER INFORMATION: polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCCAGGGCTTGCCGGGGCCGA--TGGCCGCGACGGCCGCGACGGCGCCCCGGGGCTC
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                                                                                                               TTTTCGGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGGGGCCATGGTGAGGCTGGAGC
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TCAAGACAGCAGCACCTTCTCCGGATTTCTGGTGTA
                              AY CARGTNTGGGTNMGNYTNTAYAARGGNGARMGNGARAAY GCNATHTTYW SNGARGARY
                                                          CTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTACATTGGCATCTATGCCAGCA
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US-09-506-855-23
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; NAME/KBY: variation
; LOCATION: (1)...(843)
; OTHER INFORMATION: Each N is independently any nucleotide
US-09-506-855-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.6%; Score 77.4; DB 4; Length 843; Best Local Similarity 30.0%; Pred. No. 3e-07; Matches 209; Conservative 99; Mismatches 384; Indels
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Patent No. 644822
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CURRENT FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 23
LENGTH: 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sheppard, Paul O.
APPLICANT: Lasser, Gerald W.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS
TITLE OF INVENTION: IMMUNE FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 99-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Degenerate nucleotide sequence encoding zsig37
OTHER INFORMATION: polypeptide
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AGTICACCIGCCAGGIGCCIGGGGICTACTICGCCGICCAIGC---CACCGICIACC 707
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                                             ARAARGARACNTAYYTNCAYATHATGAARAAYGARGARGARGTNGTNATHYTNTTYGCNC
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ARGTNGGNGAYMGNWSNATHATGCARWSNCARWSNYTNATGYTNGARYTNMGNGARCARG

Search completed: June 20, 2003, 08:45:34 Job time: 107 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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1: /cgn2_6/ptodata/2/pubpna/US07_1: /cgn2_6/ptodata/2/pubpna/PCT_N_1: /cgn2_6/pt
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                                         syn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
syn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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Result	Score	Query Match	Length [Bd	ID	Description
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N	1377	100.0	1377	9	US-09-944-403-41	Sequence 41, Appl
w	1377	100.0	1377	9	US-09-944-896-41	Sequence 41, Appl
4	1377	100.0	1377	9	US-09-944-944-41	•
v	1377	100.0	1377	9	US-09-944-907-41	-
σ	1377	100.0	1377	9	US-09-944-929-41	-
7	1377	100.0	1377	9	US-10-028-072-361	
œ	1377	100.0	1377	9	US-10-121-049-361	Sequence 361, App
9	1377	100.0	1377	9	US-10-123-904-361	
10	1377	100.0	1377	9	US-10-140-470-361	
11	1377	100.0	1377	9	US-10-175-746-361	
12	1377	100.0	1377	9	US-10-176-918-361	
13	1377	100.0	1377	9	US-10-176-921-361	Sequence 361, App
14	1377	100.0	1377	9	US-10-137-865-361	
15	1377	100.0	1377	9	US-10-140-474-361	
16	1377	100.0	1377	9	US-10-142-431-361	
17	1377	100.0	1377	9	US-10-143-114-361	
18	1377	100.0	1377	9	US-10-140-002-361	Sequence 361, App
19	1377	100.0	1377 .	٥	10 10 110 110	

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Sequence 3		Sequence 3	Sequence 3	Sequence 3	Sequence 3	Sequence 3	Sequence 4	Sequence 3	Sequence 3	Sequence 3	Seguence 30	Sequence 30		Sequence 30	Sequence 30		Sequence 36	Sequence 36	Sequence 36	Sequence 36				
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ALIGNMENTS

1 944-413-41 ence 41, Application US/09944413 ence 41, Application US/09944413 ent No. US20020156004A1 rRAL INFORMATION: LICANT: Baker, Kevin LICANT: Betetein, David LICANT: Betetein, David LICANT: Betern, Many LICANT: Gerritsen, Many LICANT: Goddard, Audrey LICANT: Goddard, Audrey LICANT: Goddard, Audrey LICANT: Goddard, Christopher LICANT: Roy, Margaret LICANT: Tumas, Daniel LICANT: Roy, Margaret LICANT: NOGO, William LR OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND LR OF INVENTION: ACIDS ENCODING THE SAME E REFERENCE: P2546712 RENT FILING DATE: Docember: 05/067/44,413 RENT FILING DATE: Docember: 05/067/44,413 RENT FILING DATE: Docember: 11, 1997 OR APPLICATION NUMBER: 60/069,334 OR FILING DATE: Docember: 11, 1997 OR APPLICATION NUMBER: 60/069,334 OR FILING DATE: Docember: 11, 1997 OR APPLICATION NUMBER: 60/069,278 OR FILING DATE: Docember: 11, 1997 OR APPLICATION NUMBER: 60/069,425 OR FILING DATE: Docember: 11, 1997 OR APPLICATION NUMBER: 60/069,696 OR FILING DATE: Docember: 16, 1997 OR APPLICATION NUMBER: 60/069,696 OR FILING DATE: Docember: 16, 1997 OR APPLICATION NUMBER: 60/069,696 OR FILING DATE: Docember: 16, 1997 OR APPLICATION NUMBER: 60/069,696	[*]	٠.			٠.	٠.	٠.	٠.	٠.	٠.	٠.	٠.	٠.	٠.	٠.	٠.	٠.	٠.	٠.	٠.	٠.	••	••	٠.	٠.		•••	••	••	••	••	٠.	٠.	٠.		•••		S	RE
Application US/09944413 REMATION: Baker, Kevin Botstein, David Eaton, Dan Perrara, Mapoleone Filvaroff, Ellen Gerritsen, Mary Goddard, Audrey Godowski, Paul Grimaldi, Christopher Gurney, Austin Hillan, Kenneth Kljavin, Ivar Napier, Mary Roy, Margaret Tumas, Daniel WCANTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TVENTION: SECRETED AND TRANSMEMBRANE MCE: P2548P1C1 WCOO,William TVENTION: SECRETED AND TRANSMEMBRANE MCE: P2548P1C1 SICATION NUMBER: US/09/944,413 LICATION NUMBER: 09/866,028 GOATE: December 3, 1997 CCATION NUMBER: 60/069,334 GG DATE: December 11, 1997 CCATION NUMBER: 60/069,334 GG DATE: December 11, 1997 CCATION NUMBER: 60/069,335 GG DATE: December 11, 1997 CCATION NUMBER: 60/069,425 GG DATE: December 11, 1997 CCATION NUMBER: 60/069,694 GG DATE: December 11, 1997 CCATION NUMBER: 60/069,694 GG DATE: December 11, 1997 CCATION NUMBER: 60/069,694 GG DATE: December 16, 1997	PRIOR PRIOR	PRIOR			CURREN	CURREN	FILE F	TITLE	TITLE	APPLIC	APPLIC	APPLIC	APPLIC	APPLIC	APPLIC	APPLIC	APPLIC	APPLIC	APPLIC	APPLIC	APPLIC	APPLIC	APPLIC	APPLIC	APPLIC	GENERAL	Sequenc	-09-944	RESULT 1										
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413 TRANSMEMBRANE POLYPEPTIDES AND ING THE SAME 9/944,413 ,028 ,028 ,1997 ,334 ,1997 ,1997 ,278 ,1997 ,694 ,694	TION NU	DATE: [_ '	DATE: E	DATE: D	TION NO	DATE: D	_			DATE: D	TION NU	DATE: 2	TION NU	G DATE:	CATION	E: P254	NTION:	NTION:	ood, Wil	umas, Da	oy, Marg	apier, M	ljavin,	illan, K	urney, A	rimaldi	odowski	oddard,	erritse	ilvarof	errara,	aton, Da	otstein	ker, Ke	ATION:	0020156 DDIICac	;	
413 TRANSMEMBRANE POLYPEPTIDES AND ING THE SAME 9/944,413 ,028 ,028 ,1997 ,334 ,1997 ,1997 ,278 ,1997 ,694 ,694	MBER: 6	ecember	MBER: 6	ecember	ecember	MBER: 6	001-05-	MBER: 0	2001-	NUMBER:	8P1C1	ACIDS	SECRETE	liam	niel	aret	ary	Ivar	enneth	ustin	,Christ	, Paul	Audrey	n, Mary	f,Ellen	Napoleo	ם	,David	vin		10D US/								
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QY 1 GACTAGTTCTCTTGGAGTCTGGGAGGGAAGGGGAAGGCGGAGGCAGGGAGCGAGGACCAGGAC 60	Query Match 100.0%; Score 1377; DB 9; Length 1377; Best Local Similarity 100.0%; Pred. No. 0; Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	NGTH: PE: DN CANISM 944-41	; PRIOR APPLICATION NUMBER: PCT/US01/06520 ; PRIOR FILING DATE: February 28, 2001 ; NUMBER OF SEQ ID NOS: 120 ; SEQ ID NO 41	APPLICATION NUMBER: FILING DATE: July 28 ARPLICATION NUMBER: FILING DATE: Decembe	; PRIOR APPLICATION NUMBER: PCT/US00/08439 ; PRIOR FILING DATE: March 30, 2000 ; PRIOR FILING DATE: MORER: PCT/US00/14042 ; PRIOR FILING DATE: MAY 22, 2000	; PRIOR APPLICATION NUMBER: PCT/US00/04414 ; PRIOR FILING DATE: February 22, 2000 ; PRIOR FILING DATE: March 2, 2000 ; PRIOR FILING DATE: March 2, 2000	APPLICATION N FILING DATE: APPLICATION N FILING DATE:	NUMBER: PCT/US99/28313 No. US20020156004A1ember 30, NUMBER: PCT/US99/28301 December1, 1999	APPLICATION I FILING DATE: APPLICATION I FILING DATE:	APPLICATION I FILING DATE: APPLICATION I FILING DATE:	APPLICATION FILING DATE APPLICATION FILING DATE	APPLICATION NUMBER: P FILING DATE: Septembe APPLICATION NUMBER: P FILING DATE: December	APPLICATION NUMBER: 6 FILING DATE: December APPLICATION NUMBER: 6 FILING DATE: July 28.	APPLICATION NUMBER: 6 FILING DATE: February APPLICATION NUMBER: 6 FILING DATE: December	APPLICATION NUMBER: 60/0 FILING DATE: February 9, APPLICATION NUMBER: 60/0 FILING DATE: February 9.	APPLICATION NUMBER: 60/061 FILING DATE: December 18, APPLICATION NUMBER: 60/071 EILING DATE: January 5, 11	0/069 17, 0/069	; PRIOR APPLICATION NUMBER: 60/069,702 ; PRIOR FILING DATE: December 16, 1997
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1081 GCACTCTCCGTCCTGCTGCCAGGCAAGGAATGGGAACAGTGGCTGTCTGCGATCAGGTCTG 1140	1 GGTCATCCAGGAGGGCTGGCCCCCTGGAATATTGTGAATGACTAGGCAGGTGGGGTAGA	961 CCCACTGCAAAGTGAGCTCATGCTCTCACTCCTAGAAGGAGGGTGTGAGGCTGACAACCA 1020 	901 CACCTTCTCCGGATTTCTGGTGTACTCCGACTGGCACAGCTCCCCAGTCTTTGCTTAGTG 960	841 GTGGGTGCAGGTGGGTGAGGTGACTACATTGGCATCTATGCCAGCATCAAGACAGAC	781 GCCCAAGCCAGCCTCGCTCTCGGGGGGGGGGGCCATGGTGAGGCTTGAGGCCTGAGGCCTGAGGCCAAGT 840	721 GITTGAICTGGTGAAGAATGGCGAATCCAITGCCTCTTTCTTCCAGTITTTTCGGGGGGGTG 780 	661 CCAGGIGCCTGGGGTCTACTACTTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCA 720	601 CGACCGCGTGCTGGTGAACGAGCAGGGACATTACGACGCCGTCACCGGCAAGTTCACCTG 660	541 CTTCAGCGCCAAGCGCTCCGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCTTGCCCTT 600	481 GGCGGGACCCGCGGGGCCTGCCGGGGATGCTCGGTGCCTCCGCGATCCGC 540	421 AGGCGAGGGCGGGAGGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAAA 480	361 CTTGCCGGGCCGCGATGGCCGCGACGGCGCGCGCGCGGGGGCTCCGGGAGAGAA 420	301 CAGCCTCTGCCCGGGGCACCCCGGCCTTCCAGGCACGCCGGGCCACCATGGCAGGG 360	241 CGTCCTGCTGCTCCTGGGCCTGGCGGCTCGCCCCACTGGACGACAACAAGATCCC 300 	181 GGACTGCGAGAGAACCCCGGGGTCCGGGGCTCCCGGTGCCAATGAGGCCACTCCT 240	121 CCAACTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGG 180	61 TGGGGTGACGGCAGGGCAGGGGGCCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCA 120	1 GACTAGTTCTCTTGGAGTCTGGGAGGAAGGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGAC 60

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,403
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR PILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/669,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/69335
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TITLE OF IN
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& FILING DATE: December 12, 1997
& APPLICATION NUMBER: 60/069,696
& APPLICATION NUMBER: 60/069,696
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FILING DATE: December 16
APPLICATION NUMBER: 60/069,694
FILING DATE: December 16
                                                                FILING DATE: December 17, 1997
APPLICATION NUMBER: 60/068,017
FILING DATE: December 18, 1997
APPLICATION NUMBER: 60/070,440
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APPLICATION NUMBER: 60/069,702
FILING DATE: December 16, 1997
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                                                                                                                                                      FILING DATE: December 1
APPLICATION NUMBER: 60,
FILING DATE: December 1
                               APPLICATION NUMBER: 60/074,
                                                                                                                     APPLICATION NUMBER: 60/069,873
FILING DATE: December 17, 1997
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o. US20020165143A1
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Tumas, Daniel
Wood, William
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Grimaldi, Christopher
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Napier,Mary
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Best Local Similarity
Matches 1377; Conserv
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TYPE: DNA
ORGANISM: Homo Sapien
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FILING DATE: December 22, 1998
APPLICATION NUMBER: 09/254,311
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APPLICATION NUMBER: 60/075,945
FILING DATE: February 25, 1998
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PRIOR APPLICATION NUMBER: PCT/US98/19330
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APPLICATION NUMBER: PCT/US01/06520
FILING DATE: February 28, 2001
R OF SEQ ID NOS: 120
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APPLICATION NUMBER: PCT/US00/20710
FILING DATE: July 28, 2000
APPLICATION NUMBER: PCT/US00/32678
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APPLICATION NUMBER: PCT/US00/08439
FILING DATE: March 30, 2000
APPLICATION NUMBER: PCT/US00/14042
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
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APPLICATION NUMBER: PCT/US98/25108
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APPLICATION NUMBER: PCT/US00/04414
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APPLICATION NUMBER: PCT/US99/30095
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GGGACTGCGAGAGGACCCCGGGGTGCCGGGGCTCCAGCGCTATGAGGCCACTCCT 240
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                                                                         CCAACTGGAGGGTCCGGAGTAGCGAGCGCCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGG
                                                                                                   CCAACTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCCGGGAGGG
                                                                                                                                                                         TGGGGTGACGGCAGGGCAGGGGGCGCCTGGCCCGGGGAGAAGCGCCGGGGGGCTTGGAGCACCA 120
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Pred. No. 0;
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                               GGTCATCCAGGAGGGCTGGCCCCCCTGGAATATTGTGAATGACTAGGGAGGTGGGGTAGA
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CURRENT APPLICATION NUMBER: US/09/944,896
CURRENT APPLICATION NUMBER: US/09/944,896
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR PRIOR PLING DATE: 2001-05-25
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR PPLICATION NUMBER: 60/069,696
PRIOR PILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR PILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR PILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
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PRIOR APPLICATION NUMBER: 60/069,870
PRIOR PILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR APPLICATION NUMBER: 60/069,873
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PRIOR APPLICATION NUMBER: 60/070,440
PRIOR APPLICATION NUMBER: 60/074,409
PRIOR APPLICATION NUMBER: 60/074,409
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Patent No. U
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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Tumas, Daniel
Wood, William
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Grimaldi, Christopher
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; LENGTH: 1377
; TYPE: DNA
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OR APPLICATION NUMBER: PCT/US99/21090
OR APPLICATION SEPTEMBER: PCT/US99/28409
OR FILING DATE: NO. US20020168715Alember 30
OR APPLICATION NUMBER: PCT/US99/2813
OR APPLICATION NUMBER: PCT/US99/28301
OR APPLICATION NUMBER: PCT/US99/28301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OR FILING DATE: February 22, 2000
OR APPLICATION NUMBER: PCT/USO0/05841
OR FILING DATE: March 2, 2000
OR APPLICATION NUMBER: PCT/USO0/08439
OR FILING DATE: March 30, 2000
OR APPLICATION NUMBER: PCT/USO0/14042
OR FILING DATE: May 22, 2000
OR APPLICATION NUMBER: PCT/USO0/20710
OR APPLICATION NUMBER: PCT/USO0/20710
OR FILING DATE: July 28, 2000
OR FILING DATE: July 28, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US00/32678
FILLING DATE: December 1, 2000
APPLICATION NUMBER: PCT/US01/06520
FILLING DATE: February 28, 2001
R OF SEQ ID NOS: 120
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APPLICATION NUMBER: PCT/US00/03565
FILING DATE: February 11, 2000
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APPLICATION NUMBER: 09/254,311
FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
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APPLICATION NUMBER: PCT/US99/30095
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APPLICATION NUMBER: PCT/US00/04414
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 AGGCGAGGGCGGGAACTGCCGGGACTCGAGGGGACCCCGGGCCGCGAGGAGA
                                                              CTTGCCGGGCCGCGATGGCCGCGCGCGCCCCGGGGCCCCGGGGAGAGAA
                                                                                                                          CAGCCTCTGCCCGGGGCACCCCGGCCTTCCCAGGCACGCCGGGCCACCATGGCAGCCAGGG
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; Sequence 41, Application US/09944944
patent No. US20020173463A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
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FILE REFERENCE: P2548PLC1
CURRENT APPLICATION NUMBER: US/09/944,944
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
PRIOR PILING DATE: December 3,1997
PRIOR PILING DATE: December 11, 1997
PRIOR PILING DATE: December 11, 1997
PRIOR PILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,325
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR PILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,25
PRIOR PILING DATE: December 12, 1997
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                                                                                  OR FILING DATE: December 22, 1998
OR APPLICATION NUMBER: 09/254,311
OR FILING DATE: MATCH 3, 1999
OR APPLICATION NUMBER: PCT/US99/12252
OR FILING DATE: June 22, 1999
OR APPLICATION NUMBER: PCT/US99/21090
OR APPLICATION NUMBER: PCT/US99/21090
OR FILING DATE: September 15, 1999
OR FILING DATE: September 15, 1999
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APPLICATION NUMBER: PCT/US99/28409 FILING DATE: No. US20020173463A1ember 30, APPLICATION NUMBER: PCT/US99/28313 FILING DATE: No. US20020173463A1ember 30, APPLICATION NUMBER: PCT/US99/28301
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APPLICATION NUMBER: 60/146,222
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Hillan, Kenneth
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Grimaldi, Christopher
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Goddard, Audrey
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Roy, Margaret
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                                                                                                                                                        N NUMBER: 09/218,517
B: December 22, 1998
N NUMBER: 09/254,311
B: March 3, 1999
                                                                                                                                                                                                                                                                                                            NUMBER: 60/146,222
: July 28, 1999
NUMBER: PCT/US98/19330
                                                                                                                                                                                                                                                                                                                                                                                : December 16, 1998
NUMBER: 60/113,296
                                                                                                                                                                                                                                            NUMBER: 09/
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NUMBER: 60/075,945
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US-09-944-944-41
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APPLICATION NUMBER: PCT/US00/08439
FILING DATE: March 30, 2000
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FILING DATE: December 1, 2000
APPLICATION NUMBER: PCT/US01/06520
FILING DATE: February 28, 2001
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FILING DATE: May 22, 2000
APPLICATION NUMBER: PCT/US00/20710
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APPLICATION NUMBER: PCT/US00/04414
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APPLICATION NUMBER: PCT/US00/03565
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              CGACCGCGTGCTGGTGAACGAGCAGGAGGACATTACGACGCCGTCACCGGCAAGTTCACCTG
                                                                                      CTTCAGCGCCAAGCGCTCCGAGAGCCGGGTGCCTTCCGCCGTCTGACGCACCCTTTGCCCCTT
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Tumas, Daniel
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Grimaldi, Christopher
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Goddard, Audrey
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; CURRENT APPLICATION NUMBER: US/09/944,90
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
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Query Match 100.0%; Score 1377; DB 9; Length 1377; Best Local Similarity 100.0%; Pred. No. 0;	Homo Sapien	PRIOR FILING NOTICE: 07/000,020 PRIOR FILING DATE: 2001-05-25 NUMBER OF SEQ ID NOS: 120 SEQ ID NO 41 LENGTH: 1377	; TITLE OF INVENTION: ACIDS ENCODING THE SAME ; FILE REFERENCE: P2548P1C1 ; CURRENT APPLICATION NUMBER: US/09/944,929 ; CURRENT FILING DATE: 2001-08-31 ; CURRENT FILING DATE: 2001-08-31	CANT: CANT: CANT:			Botste Eaton, Ferrar	; Sequence 41, Application US/09944929; Publication No. US20020197612A1; GENERAL INFORMATION:	RESULT 6 US-09-944-929-41	Qy 1321 GATCACTCAATAAACCTAAGAACCCTCATAAAAAAAAAA	Qy 1261 CTCTGCTTCTCTGGATCCTCCCCACCCCCTCCTGCTGCGGGCCCGTTTTCTCAGA 1320	Oy 1201 GTGTAAGTCCCCCAGTTGCTCTGGTCCAGGAGCCCACGGTGGGGTGCTCTCCTTCCT	QY 1141 GCAGCATGGGGCAGTTGGCTGGATTTCTGCCCAAGACCAGAGGAGTGTGCTGTGTTGCCAA 1200	QY 1081 GCACTCTCCGTCCTGCTGCCAAGGAATGGGAACAGTGGCTGTCTGCGATCAGGTCTG 1140	OY 1021 GGTCATCCAGGAGGGCTGGCCCCCTGGAATATTGTGAATGACTAGGGAGGTGGGGTAGA 1080	OY 961 CCCACTGCAAAGTGAGCTCATGCTCTCACTCCTAGAAGGAGGGTGTGAGGCTGACCAACCA	Qy 901 CACCTTCTCCGGATTTCTGGTGTACTCCGACTGGCACAGCTCCCCAGTCTTTGCTTAGTG 960	Db 841 GTGGGTGCAGGTGTGGGTGACTACATTGGCATCTATGCCAGCATCAAGACAGAC
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PRIOR FILING DATE: 1997-09-17 PRIOR APPLICATION NUMBER: 60/059184 PRIOR APPLICATION NUMBER: 60/059263 PRIOR PILING DATE: 1997-09-17 PRIOR PILING DATE: 1997-09-18 PRIOR PILING DATE: 1997-09-18 PRIOR PILING DATE: 1997-09-19 PRIOR APPLICATION NUMBER: 60/059588 PRIOR PILING DATE: 1997-09-19 PRIOR APPLICATION NUMBER: 60/059886 PRIOR PILING DATE: 1997-09-19 PRIOR APPLICATION NUMBER: 60/059836 PRIOR PILING DATE: 1997-09-24 PRIOR APPLICATION NUMBER: 60/062250 PRIOR PILING DATE: 1997-10-17 PRIOR PILING DATE: 1997-10-17 PRIOR APPLICATION NUMBER: 60/062285	APPLICATION NUMBER: 6 FILING DATE: 1997-06- APPLICATION NUMBER: 6 FILING DATE: 1997-08- APPLICATION NUMBER: 6 FILING DATE: 1997-09- APPLICATION NUMBER: 6	222 00000000000000000	RESULT 7 (Sequence 361, Application US/10028072) (Publication No. US20030004311A1) (GENERAL INFORMATION: (APPLICANT: Baker, Kevin P. (APPLICANT: Beresini, Maureen (APPLICANT: DeForge, Laura (APPLICANT: DeForge, Laura (APPLICANT: Desnoyers, Luc	1081 GCACTCTCCGTCCTGCTGGCAAGGAATGGGAACAGTGGCTGTCTGCGATCAGGTCTG 1140
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Db 1 GACTAGTTCTCTTGGAGTCTGGGAGGAAGGGAAGCGGAGCGAACCAGGAC 60	QY . 1 GACTAGTTCTTGGAGTCTGGGAGGAAGGGAAGGGGAGGGA	Query Match 100.0%; Score 1377; DB 9; Length 1377; Best Local Similarity 100.0%; Pred. No. 0; Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	NGTH: PB: DN CANISM 121-04	ILING DATE: 2002-(r Application remov SEQ ID NOS: 550 361		APPLICANT: APPLICANT: APPLICANT:	APPLICANT: Groupski, Faul O. APPLICANT: Sherwood, Steven APPLICANT: Smith, Victoria APPLICANT: Smith, Victoria	APPLICANT: Gao, Wei-Qiang APPLICANT: Gerritsen, Mar APPLICANT: Goddard, Audre	APPLICANT: APPLICANT: APPLICANT:	Sequence 361, Application US/10121049 ; Sequence 361, Application US/10121049 ; Publication No. US20030022239A1 ; GENERAL INFORMATION: ADDITION: BAKEY KEYIN D	SULT 8	Qy 1321 GATCACTCAATAAACCTAAGAACCCTCATAAAAAAAAAA	OY 1261 CTCTGCTTCTCTGGATCCTCCCACCCCCTCCTGCTGCGGCCCCTTTTCTCAGA 1320	OY 1201 GTGTAAGTCCCCCAGTTGCTCTGGTCCAGGAGCCCACGGTGGGGTGCTCTCTTCCTGGTC 1260 Db 1201 GTGTAAGTCCCCCAGTTGCTCTGGTCCAGGAGCCCACGGTGGGGTGCTCTCTTCCTGGTC 1260	OY 1141 GCAGCATGGGGCAGTTGGCTGGATTTCTGCCCAAGACCAGAGGAGTGTGCTGTGCTGGCAA 1200	OY 1081 GCACTCTCCGTCCTGCTGCCAAGGAATGGGAACAGTGGCTGTCTGCGATCAGGTCTG 1140	1021 1021	QY 961 CCCACTGCAAAGTGAGCTCATGCTCTCACTCCTAGAAGGAGGGTGTGAGGCTGACAACCA 1020
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Db 61 TGGGTTGACGGCAGGGCAGGGCCCTGGCCGGGGAAGAACGGCGAGGAGGACACCACTCCT 240 Qy 121 CCAACTGGAAGGACCCCGGGAGTAGCGGCGAAGAAGACCCCGAAGAAGACCCCGAAGAAGACCCCGAAGAA	Query Match 100.0%; Score 1377; DB 9; Length 1377; Best Local Similarity 100.0%; Pred. No. 0; Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 GACTAGTTCTCTTGGAGTCTGGGAGGAAGCGAGCCGAGC	FILING DATE: 2002-(pplication removed - pplication resoved - OF SEQ ID NOS: 550 O 361 : 1377 : 1377 DNA SM: Homo Sapien 904-361	APPLICANT: Schwat, Indicity A. APPLICANT: Tumas, Daniel APPLICANT: Watanabe, Colin K APPLICANT: Wood, William APPLICANT: Wood, William TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C54 CHERRET APPLICATION NUMBER: US/10/123.904	Filvarott, Ellen Gao, Wei-Qiang Gerritsen, Mary Geoddard, Audrey Goddwski, Paul J. Gurney, Austin L. Sherwood, Steven Smith, Victoria	US-10-123-904-361 ; Sequence 361, Application US/10123904 ; Publication No. US20030022328A1 ; Publication No. US20030022328A1 ; GENERAL INFORMATION: ; APPLICANT: Baker, Kevin P. ; APPLICANT: Beresini, Maureen ; APPLICANT: DeForge, Laura ; APPLICANT: Desnoyers, Luc	Db 1261 CTCTGCTTCTCGATCCTCCCACCCCTCCTGCTCCTGGGGCCGGCC	Db 1141 GCAGCATGGGGCAGTGGCTGGATTTCTGGCCCAAGACCAGAAGGAGTGTGCTTCTGGCAA 1200 Qy 1201 GTGTAAGTCCCCCAGTTGCTCTGGTCCAGGACCCAAGAGGAGTGGGTCTCTTCCTGGTC 1260 Db 1201 GTGTAAGTCCCCCAGTTGCTCTGGTCCAGGAGCCCACGGTGGGGTGCTCTTCCTGGTC 1260 Db 1201 GTGTAAGTCCCCCAGTTGCTTCTGGTCCAGGAGCCCACGGTGGGGTGCTCTTCCTGGTC 1260 Qy 1261 CTCTGCTTCTCTGGATCCTCCCCACCCCCTCCTGGTGCTGCTGGGCCCGTTTTCTCAGA 1320
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
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Watanabe, Colin K
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Gao, Wei-Qiang
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Desnoyers, Luc
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                                    Sequence 361, Application US/10175746
Publication No. US20030027270A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
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DeForge, Laura
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Gao, Wei-Qiang
Gerritsen, Mary E.
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Query Match Best Local S Matches 1377

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US-10-175-746-361
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT FILING DATE: 2002-06-19
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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                                                                       APPLICANT:
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APPLICANT: Beresini, Maur
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
                         TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C382
                                                                                                                                    APPLICANT:
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
                                                                                    Tumas, Daniel
Watanabe, Colin K
Wood, William
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Gerritsen, Mary E.
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Filvaroff, Ellen
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              NUMBER: US/10/176,918
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LENGTH: 1377
TYPE: DNA
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US-10-176-921-361
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Publication No. US20030027276A1
Query Match
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                                                                                                                      APPLICANT: Zhang, Zemin TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C288

CURRENT APPLICATION NUMBER: US/10/176,921

CURRENT FILING DATE: 2002-06-20
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Desnoyers, Luc
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 100.0%; ilarity 100.0%; Conservative 0
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Qy 181 GGGACTGCGAGAGGACCCCGGGGTCCCGGGGTGCCAGCGCTATGAGGCCACTCCT		
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Query Match 100.0%; Score 1377; DB 9; Length 1377; Best Local Similarity 100.0%; Pred. No. 0; Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps		841 GTGGGTGCAGGTGGGTGTGGGTGACTACATTGGCATCTATGCCAGCATCAAGACAGAC
; IYES: DNA ; ORGANISM: Homo Sapien US-10-137-865-361		781 GCCCAAGCCAGCCTCTCGGGGGGGGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGT 840
; FIOT Application removed - See Palm or File Wrapper ; NUMBER OF SEQ ID NOS: 550 ; SEQ ID NO 361 ; LENGTH: 1377		721 GTTTGATCTGGTGAAGAATGGCGAATCCATTGCCTCTTTCTT
FILE REFERENCE: P330RIC154 CURRENT APPLICATION NUMBER: US/10/137,865 CURRENT FILING DATE: 2002-05-03		661 CCAGGTGCCTGGGGTCTACTACTTCGCCGTCCATGCCACCGTCTACCGGGGCCAGCCTGCA 720
APPLICANT: Wood, William APPLICANT: Wood, William APPLICANT: Zhang, Zemin TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC		601 CGACCGCTGCTGGTGAACGAGCAGGGACATTACGACGCCGTCACCGGCAAGTTCACCTG 660
APPLICANT: SHERWOOD, SEEVEN APPLICANT: Stewart, Timothy A. APPLICANT: Stewart, Timothy A. APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel		541 CTTCAGCGCCAAGCGCTCCGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCTTTGCCCTT 600
		481 GGCGGGACCCGCGGGCCCACCGGGCCTGCCGGGGATCCTCCGCTGCCGCGATCCGC 540
DeFormation DeFormation Designation Designation DeFormation DeForm		421 AGGCGAGGGCGGGAGGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGA 480
ORMATI Baker Bere		361 CTTGCCGGGCCGCGATGGCCGCGACGGCCGCGACGGCCCCGGGGGCTCCCGGGAGAGAA 420
RBSULT 14 US-10-137-865-361 ; Sequence 361, Application US/10137865		301 CAGCCTCTGCCCGGGGCACCCCGGCCTTCCAGGGACGCCGGGCCACCATGGCAGGG 360
ОУ 1321 GATCACTCAATAAACCTAAGAACCCTCATAAAAAAAAAA		241 CGTCCTGCTGCTCCTGGGCCTGGCGGCCGGCTCGCCCCACTGGACGACAACAAGATCCC 300
1261 CTCTG		181 GGGACTGCGAGAGGACCCCGGCGTCCGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCT 240
1201 GTGTA	,	121 CCAACTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGG 180
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Db 241		
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Db 181		081
Qy 181	114	1081 GCACTCTCCGT
Db 121	GGTCATCCAGGAGGCTGGCCCCCCTGGAATATTGTGAATGACTAGGGAGGTTGGGTTAGA 1080	021
Фу 121		1021 GGTCATCCAGG
Db 61	CCACTGCAAAGTGAGCTCATGCTCTCACTCCTAGAAGGAGGGTGTGAGGCTGACAACCA 1020	61
Qy 61	3 6	
Db 1		
97		901 CACCTTCTCCG
Query Match Best Local (Matches 137)	GTGGGTGCAGGTGGGTGTGGGTGACTACATTGGCATCTATGCCAGCATCAAGACAGAC	841 GTGGGTGCAGG
; ORGANISM: US-10-140-474	GCCCAAGCCACCTCGCTCTCGGGGGGGGCCATGGTGAGGCCTGAGGACCAAGT 840	781 GCCCAAGCCAG 781 GCCCAAGCCAG
; LENGTH: 1	#ANGAAIGGCGAAICCAINGCCICITICCAGITITITCGGGGGGGTG 780	
; SEQ ID NO 3	GTTTGATCTGGTGAAGAATGGCGAATCCATTGCCTCTTTCTT	
CURRENT FI	STCTACTACTTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCA 720	661 CCAGGTGCCTG
; FILE REFER	CCAGGTGCCTGGGGTCTACTACTTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCA 720	661 CCAGGTGCCTG
	GTGAACGAGGACATTACGACGCCGTCACCGGCAAGTTCACCTG 660	601 CGACCGCGTGC
APPLICANT:	CGACCGCGTGCTGGTGAACGAGCAGGACATTACGACGCCGTCACCGGCAAGTTCACCTG 660	601 CGACCGCGTGC
APPLICANI:	GCCTCCGAGAGCCGCGTCCGCCGTCTGACCCATCCCTTCCCCCTT 600	541 CTTCAGCGCCA
; APPLICANT:	CTTCAGCGCCAAGCGCTCCGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCTTGCCCCTT 600	541 CTTCAGCGCCA
; APPLICANT:	GCGGGACCCGCGGGCCCACCGGGCCTGCCGGGGATCCGCTCCGCCATCCGCC 540	481 GGCGGGACCCG
; APPLICANT:	GGGGCCACCGGGCCTGCCGGGGAGTGCTCCGTGCCTCCGCGATCCGC 540	481 GGCGGGACCCG
; APPLICANT:	AGGCGAGGCGGGAACGCCGGGACCTCGAGGGGACCCCCGGGCCGAGGAGA 480	421 AGGCGAGGGCG
; APPLICANT:	GAGGCCGGGACTGCCGGGACCTCGAGGGGGACCCCCGGGCCGCGAGGAGA 480	
; APPLICANT:	CTTGCCGGGCCGCGATGGCCGCGACGGCCGCGACGGCGCGCGC	161 CTTGCCGGGCC
; Publication ; GENERAL INF	CGATGGCCGCGACGGCGCGCGCCCCGGGGCTCCGGGAGAGAA 420	361 CTTGCCGGGCC
US-10-140-474 ; Sequence 36		
Db 1321		
Оу 1321		241 CGTCCTGCTGC

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INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC INVENTION: ACIDS ENCODING THE SAME INVENTION: ACIDS ENCODING THE SAME SRENCE: P3330R1C152

IPPLICATION NUMBER: US/10/140,474

FILING DATE: 2002-05-06

FILING DATE: 2002-05-06

FILING DATE: 2002-05-06
 h 100.0%; Score 1377;
Similarity 100.0%; Pred. No. 0;
77; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FORMATION:
: Baker, Kevin P.
                                                                                                                                                   SEQ ID NOS: 550
                                                                                 Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                 Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
                                                                                                                                                                                                                                                                                   Tumas, Daniel
Watanabe, Colin K
Wood, William
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Stewart, Timothy A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Desnoyers, Luc
Filvaroff, Ellen
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DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/10140474 o. US20030032156A1
 0; Mismatches
                                DB 9;
 0;
                                Length 1377;
   Indels
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1321 GATCACTCAATAAACCTAAGAACCCTCATAAAAAAAAAA	1261 CTCTGCTTCTCGGATCCTCCCACCCCTCCTGCTCCTGGGGCCCGGCCCTTTTCTCAGA 1320	1201 GTGTAAGTCCCCCAGTTGCTCTGGTCCAGGAGCCCACGGTGGGGTGCTCTCTTTCCTGGTC 1260	1141 GCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACCAGAGGAGTGTGCTGTGCTGGCAA 1200 	1081 GCACTCTCCGTCCTGCTGCTGCCAAGGAATGGGAACAGTGGCTGTCTGCGATCAGGTCTG 1140 	1021 GGTCATCCAGGAGGGCTGGCCCCCCTGGAATATTGTGAATGACTAGGGAGGTGGGGTAGA 1080 	961 CCCACTGCAAAGTGAGCTCATGCTCTCACTCCTAGAAGGAGGGTGTGAGGCTGACAACCA 1020 	901 CACCTTCTCCGGATTTCTGGTGTACTCCGACTGGCACAGCTCCCCAGTCTTTTGCTTAGTG 960	841 GTGGGTGCAGGTGGGTGTGGGTGACTACATTGGCATCTATGCCAGCATCAAGACAGAC	781 GCCCAAGCCAGCCTCTCGGGGGGGGGGGCCATGGTGAGGCTGAAGCCTGAAGCCAAGT 840 	721 GTITGAICTGGTGAAGAATGGCGAATCCATTGCCTCTTTCTTCCAGTTTTTCGGGGGGTG 780	661 CCAGGTGCCTGGGGTCTACTACTTCGCCGTCCATGCACCGTCTACCGGGCCAGCCTGCA 720	601 CGACCGCGTGCTGGTGAACGAGCAGGGACATTACGACGCCGTCACCGGCAAGTTCACCTG 660	541 CTTCAGCGCCAAGCGCTCCGAGAGCCGGGTGCCTCCGGCGTCTGACGCACCCTTGCCCTT 600	481 GGCGGGACCCGCGGGGCCCACCGGGCCTGCCGGGAATCCTCCGGCGATCCGC 540	
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Search completed: June 20, 2003, 11:21:48 Job time: 228 secs

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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compu
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AUTHORS
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              L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11475 row: i column: 07
High quality sequence stop: 777.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                            BI763193 869 bp mRNA linear EST 25-SEP-2001 603049939F1 NIH MGC_116 Homo sapiens cDNA clone IMAGE:5190222 5',
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BF055285 7j77g02.x
AI805087 tu33g05.x
AW070344 xa10d10.x
BM673416 UI-E-CR1BI688017 603315786
BM668611 UI-E-CK1BM693336 UI-E-CK1BM693336 UI-G-OT012

BF906443 IL0-OT012 BF046067 BP250014A

BI818537 603033057 BQ673882 AGENCOURT

BF098614 601750614

AW150070 xg48b05.x BE309370 601094718 BM021381 ie76e01.y

AI083823 qf18c08.x BM707291 UI-E-CR1-AI085248 qf24c09.x AI083824 qf18c09.x BE722922 191347 MA BF54023 602052317 BE138819 xw95h11.x AW192716 x150b08.x

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AF451167 AF451167 BF882978 IL3-ET011 BF724241 bx02e11.y BM966810 ij26g10.y BM966954 ij28e08.y

BM893587 ij26g10.x BM544255 AGENCOURT BI821899 603035796 BM893691 ij28e08.x

602672994 AGENCOURT BM920874 AGENCOURT BI770921 603059737

BM893691 ij28e08.x BI820945 603033989 BM021127 ie76e01.x

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/db xref="taxon:9606"
/clone="MMAGE:5190222"
/clone=1bb="NIH MGC 116"
/lab_host="DH10B"
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           Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNI)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1093)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

"Unpublished (1999)
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/lab_host="DH10B"
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db_xref="taxon:9606"
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96.8%;
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Pred. No. 4.1e-91;
0; Mismatches 24;
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Ş	유 성	р В	Q	Query M Best Lo Matches	Z	BASE COUNT					FEATURES source			COMMENT	REFERENCE AUTHORS TITLE JOHRNAL	SOURCE ORGANISM	ACCESSION VERSION	BI458455 LOCUS DEFINITION	Db I	Q	в <i>Q</i>	Db
127 GGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACT 186	67 GACGGCAGGGCAGGGGCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCAACT 126		7 TTCTCTTGGAGTCTGGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTGGGGT 66	/ Match 53.0%; Score 730.2; DB 13; Length 846; Local Similarity 96.1%; Pred. No. 1.1e-90; Local Similarity 96.1%; Pred. No. 1.1e-90; Gaps 5; Somervative 0; Mismatches 24; Indels 9; Gaps 5;		constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library." 129 a 271 c 330 g 115 t 1 others	normalized to receive the size is an and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cantramer method (Carriera in properties)	/note="0rgan: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_I: BanHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer S'-TTTTTTTTTTTTTTTTTTTTTTN-3', size-salected for average incore circ 3 the red	/clone="IMAGE:5278184" /clone_lib="NIH_MGC 96" /tlssue_type="hypothalamus" /lab_host="DH10B"	/organism="Homo sapiens" /db_xref="taxon:9606"		the distribution: MGC ci 1 through the I.M.A.G.E ://image.llnl.gov s: LLAM11702 row: j c	TOSHIYUKi and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D.	1 (bases 1 to 846) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian (bol. human. Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; E Mammalia: Rutheria: Primares: Cataryhini. Hominidae.	mRNA sequence. BI458455 BI458455.1 GI:15249111		781 GG 782	1110 TG 1111	1050 ATATTGTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGTCCTGCTGGCAAGGAA 1109	
			COMMENT	REFERENCE AUTHORS TITLE		KEYWORDS SOURCE ORGANISM	ACCESSION	RESULT 5 BI490880/c	ф	o i	 P &	da Vy	dg VQ	B &	D &	} B 8y	Db	Q B	Oy Db	Qy	Db Qy	Db
	cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be	Lumati: Cgapps-remati.nin.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc.	ished (1999) : Robert Strausberg, Ph		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	EST. BURNAN. Homo saviens		BI490880 801 bp mRNA linear BST 28-AUG	CAGGCAAGCTCGTCTCGGGGGGGGCATGTTGAGGCTGGAGCTTGAGACCAGTGTG		726 ATCTIGGTGAAGAATGGCGAATCCATTIGCCTCTTTCTTCCAGGTTTTTTCGGGGGGGTGGCCCA 785	666 TGCCTGGGGTCTACTACTTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTG 725	607 CGTGCTGGTGAACGAGCAGGGACATTACGACGCCGTCACCGGCAAGTTCACCT-GCCAGG 665	547 GGCCAAGGGTCGAGAGCGGGTGCCTCGGCGTCTGACGCACCCTTGCCCTTCGACCG 606	ACCORGAGECCA-CEGECCTECAGGAGTGCTCGGTGCTCCGCGATCCGCCTTCAG	gggcgggaAggccgggaAcTgccgggaAcCrcgaggcgaAcCcccgggccgcgAggaGacggg				247 GCTGCTCCTGGGCCTGGCCGGCCCGCCCACTGGACGACAACAAGATCCCCAGCCT 306	187 GCGAGAGGACCCCGGGGTCCGGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCCT 246	

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/db xref="taxon:9606"
/clone="IMAGE:5172880"
/clone=1bb="NIH MGC 115"
/lab_host="DH10B"
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Pred. No. 2.7e-88;
0; Mismatches 9;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 672.
Location/Qualifiers
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Plate: LLAM11513 row: o column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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603055280F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5204971 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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                     176
                                                                                                                                                                                                                        Conservative
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/db_xref="taxon:9606"
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184 c 211 g 152 t 1 others
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1045)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tisse: Procurement: Life Technologies,
                                                                                                                                                                                                                         http://image.llnl.gov
Plate: LLAM12785 row: n column:
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                                                                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                             quality sequence stop: 415.
Location/Qualifiers
                          /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:5752141"
/clone lib="NIH MGC 115"
/lab_host="DH10B"
     /note="Organ:
                                                                                                                                                          .1045
     pooled brain,
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ORIGIN
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804 934 AGGACCAAGTGTGGGTGCAGGTG-GGTGTGGGTGACTACA-TTGGCATCTATGCCA-GCA

887 696

756

TCGGTGGGTGGCCCAAACCAGCCTCGATCTCGGGGGGGGCCATGGTGATGCTGGAGCCTG

ATGACCAAGTGTGNGTGCATGTGNGGTGTGCGTGACTACATTTGTGATCTATGGCATTCA

BI770921 792 bp mRNA line: 603059737F1 NIH_MGC_122 Homo sapiens cDNA clone

linear EST 25-SEP-20 clone IMAGE:5209065 5',

EST 25-SEP-2001

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Matches
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CAGCCTGCAGTTTGATCTGGCGAAGAATGGCGAATCCATTGCCTCTTTGCTCCATGTTT
                                                                     AGTTCACCTGCCAGGTGCCTGGGGTCTACTACTTCGCCGTCCATGCCACCGTCTACCGGG
                                                                                                                                                                                                        CCTTGCCCTTCGACCGCGTGCTGGTGAACGAGCAGGGACATTACGACGCCGTCACCGGCA
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National Institutes of Health, Mammalian Gene
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Contact: Robert Strausberg, Ph.D.
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Plate: LLAM11524 row: j column:
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Tissue Procurement: Life Technologies,
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1 (bases 1 to 792)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BI770921.1 GI:15762499
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/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
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db_xref="taxon:9606"
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Pred. No. 3.5e-81;
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1 (bases 1 to 887)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
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Plate: LLAM11430 row: f column:
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                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 815.
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Clone distribution: MGC clone distribution information can
cound through the I.M.A.G.B. Consortium/LLNL at:
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/note-*Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C.
                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:5172880"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
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Homo sapiens cDNA clone IMAGE:5172880 5',
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Mammalia; Butheria; Primates; Catarrhini;
1 (bases 1 to 1623)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                       GAGGACCCCGGGCTCCGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCCTGCTG
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                        /note="Norgan: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH MGC Library." 63 a 505 c 550 g 299 t 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGB:5766864"
/clone_lib="NIH MGC 122"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                45.8%; but
100.0%; Pr
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Pred. No. 2.4e-77;
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Tissue Procurement: Miklos Palkovits,
cDNA Library Preparation: Michael J.
Toshiyuki and Piero Carninci (RIKEN)
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National Institutes of Health, Mammalian
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Mammalia; Eutheria;
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Plate: LLAM10678 row: 1 column: 23
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/db xref="taxon:9606"
/clone="IMAGE:4795558"
/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
'/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: Sall-XhoI (gtcg); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTVN-3' size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
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        Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,B., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
                                                                                                                                                                                                                                BM893587 596 bp mRNA linear EST 29-APR-2002 ij26g10.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA clone IMAGE:6136122 3' similar to TR:Q9UFX4 Q9UFX4 HYPOTHETICAL 22.8 KD PROTEIN :, mRNA sequence.
                                                                           Mammalia, Eutheria, Primates; (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by
Washington University Genome Sequencing Center For information
obtaining a clone please contact: Juliana Brown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
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Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Organ: Pancreas; Vector: pSPORT1; Site 1: Not 1; Site 2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgramm single-stranded library plasmid DNA was noxed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated
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    Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this

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/lab_host="DH10B"
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Pred. No. 2.5e-72;
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Plate: LLAM12357 row: m column: 08
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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AGENCORT 6490655 NIH_MGC_125
5', mRNA Sequence.
BM544255
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Tissue Procurement: Invitrogen
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Mammalia; Eutheria;
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
CCGGATTTCTGGTGTACTCCGACTGGCACAGCTCCCCAGTCTTTGCTTAGTGCCCACTGC
                                                                     CAGCCTCGCTCTCGGGGGGGCCATGGTGAGGCTTGGAGGCCTGAGGACCAAGTGTGGGTGC
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                                                                                                                                                                                                                                                                            138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quality sequence
                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                       /note-"Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size_2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 016."

158 c 172 g 127 t 1 others
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/lab_host="DH10B"
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99.7%;
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                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
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plate: LLAM11440 row: p column:
High quality sequence stop: 779.
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National Institutes of Health, M
Unpublished (1999)
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BI821899
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603035796F1 NIH_MGC_115
                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
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1 (bases 1 to 941)
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Bukaryota; Metazoa;
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                                                                                                                                                                                                                                         through the I.M.A.G.B. Consortium/LLNL
                                                                                               /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:5176967"
/clone lib="NIH MGC 115"
/lab_host="DH10E"
/note-*Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: ECORV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (ECORV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and
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sapiens cDNA clone IMAGE:5176967 5',
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890 AAGACAGACAGCACCTTCTCCGGATTTCTGGTGTACTCCGACTGGCACAGCTCCCCAGTC 949	830 GAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTACATTGGCATCTATGCCAGCATC 889	770 TTCGGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGGGGCCATGGTGAGGCTGGAGCCT 829	ch 42.0%; Score 578; DB 14; Length 578; 1 Similarity 100.0%; Pred. No. 7.1e-70; 578; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."	/tissue_type="Islets of Langerhans" /dev_stage="Adult" /dab_host="HildB" /lab_host="PHILDB" /lab_host="PHILDB" /note="Organ: Pancreas; Vector: pspORT1; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from	1578 /organism="Homo sapiens" /db xref="taxon:966" /clone="IMAGE:6136046" /clone ib="Melton Normalized Human Islet 4 N4-HIS 1" /sex="Both"	Tel: 617-495-1812 Tel: 617-495-8557 Email: dmelton@biohp.harvard.edu Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown (brown@fas harvard.edu) Seq primer: -40UP from Gibco High quality sequence stop: 408.	~~ K 0.5 ~ 0.6 . 5 H =	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 578) Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,	BM893691 BM893691.1 GI:19349159 EST. human. Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 199
N-PS#B;
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10-JUN-1998;
10-NOV-1998;
                                            secreted protein;
                                                                                                            Human PRO344 protein sequence
                                                                                                                                                                12-AUG-1999
                                                                                                                                                                                                                                                    AAY17827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and/or treatment (including prevention) of certain cancers, act as predictors of the prognosis of tumour treatment. Ant that bind the proteins are claimed and used in claimed cance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents human PRO344 (UNQ303), a protein encoded by the novel cDNA clone DNA40592 (see AAX87258). Amplification of DNA40592 was observed in primary lung tumours and in primary colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibody against proteins expressed tumor diagnosis and treatment
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B; AAX87258.
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                                                                 PRO protein; tumour necrosis factor family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                VFA
                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD 120
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98US-0088742.
98US-0107783.
                                               transmembrane protein; inflammation
                                                                                                                                                                                                                                                  Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 243; DB 20;
Pred. No. 4.9e-212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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                                                                    TNF; cytokine;
                                                 disorder.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes nucleic acids encoding PRO secreted and transmembrane proteins used therapeutically. The PRO proteins have cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-DEC-
16-DEC-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding PRO secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
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09-FEB-1998;
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03-DEC-1997;
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                                                                                                                                                                    VFA 243
                                                                                                                                                                                                                                                              APLPFDRVLVNBQGHYDAVTGKFTCQVPGVYYPAVHATVYRASLQFDLVKNGBSIASPFQ
                                                                                                                                                                                                                                                                                     APLPFDRYLVNEQGHYDAVTGKPTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
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97US-0069870.
97US-0069873.
97US-0068017.
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97US-0069425
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100.0%; Pred.
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and transmembrane proteins

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240 180 180 120 120 60 60 0

243; DB 20; No. 4.9e-212;

243; 0,

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Homo sapiens.

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Key
Peptide
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a protein that modulates free fatty acid metabolism. zsig39 is a member of a family of proteins having a globular domain and a collagen-like domain capable of dimerisation or oligomerisation zsig39 polypeptides were initially identified by querying an EST database for secretory signal sequences characterised by an upsti
                                                                                                                           Humes
                                                                                                                                                                              26-AUG-1998;
                                                                                                                                                                                                04-MAR-1999
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                                                             Claim
                                                                              Zsig39
                                                                                                                                            (ZYMO ) ZYMOGENETICS INC.
                                  polypeptide comprises human adipocyte-specific protein zsig39, otein that modulates free fatty acid metabolism. zsig39 is a
                                                                                                         1999-204665/17.
                                                                                                                          ž
                                                             ۲,
                                                                           protein - used to modulate fatty acid metabolism
                                                                                                AAX24684
                                                            111-112; 132pp;
                                                                                                                         Sheppard
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    peptide comprises residues 1...
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                                                                                                                                                                                                                                 "receptor binding domain"
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(specifically claimed
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Best Local S
Matches 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lung tissue library. Expression vectors, cultured cells and a method of producing zsig39 polypeptide are claimed, as well as zsig39 polypeptides having N- or C-terminal affinity tags, toxins, radionucleotides, enzymes or fluorophores, fusion proteins including zsig39 polypeptides, an antibody that specifically binds to an epitope of zsig39, and a method for modulating free fatty acid metabolism by administering a zsig39 polypeptide. The zsig39 polypeptide may also be used in organ preservation, for cryopreservation, for surgical pretreatment to prevent injury due to ischaemia and/or inflammation, and as an antimicrobial agent, promoting lysis or phagocytosis of infectious agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adipocyte complement related protein Acrp30 and adipocyte secreted protein apM1. A full-length clone (see AAX24684) was obtained from lung tissue library. Expression vectors, cultured cells and a
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AAB33461;
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Pred. No. 4.9e-21
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29-JAN-2001 (first entry)

Human protein UNQ303 SEQ ID NO:241.

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XX osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; Sjogran's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus autoimmune thrombocytopaenia; immune-mediated renal disease; demyelinating disease; hepatobiliary disease; Whipple's disease; Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective; autoimmune disease; immune-mediated skin disease; immunological disease; transplantation associated graft rejection; graft-versus-host-disease. antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic; antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; inflammatory bowel disease; gluten-sensitive enteropathy; allergic disease; mellitus;

domo sapiens.

WO200053758-A2

14-SEP-2000

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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, justen-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-1999;
                                                                                                                                                                         Sixty four PRO polypeptides, useful in the diagnosis and treatment immune related disorders, e.g. systemic lupus erythematosis, rheuma arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
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23-JUN-1999;
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Kabakoff RC,
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immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AAC58397 to AAC58578 represent PCR primers and hybridisation probes in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
                           FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
                                                                                        APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
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Pred. No. 4.9e-212;
Mismatches 0;
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standard; Protein; 243

PRO344; DNA40592-1242; human; ATCC No: 209492; antiproliferative; neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour; breast; prostate; colon; lung; renal; ovarian; central nervous system; CNS; leukemia; melanoma; Expressed Sequence Tag; EST; secreted protein;

Location/Qualifiers /label= Signal_peptide l= Mature_PRO344_protein "N-myristoylation site" "Cell attachment sequence" "N-myristoylation "N-myristoylation site"

99WO-US28409

01-DEC-1998; 98WO-US25108

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RRSULT 6
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Best Local Similarity
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22-DEC-1998;
20-JUL-1999;
26-JUL-1999;
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                                                                      PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357; PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO862; tumour cell; tumourigenesis; cancer; neoplastic cell growth; cell proliferation
                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
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                                                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                 VFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
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ilarity 100.0%;
Conservative 0
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98US-0113296.
99US-0144758.
99US-0145698.
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 Location/Qualifiers
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                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                     of novel
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                                                                                                                                                 polypeptide PRO344.
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Pred. No. 4.9e-212;
Mismatches 0;
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Query Match
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15-SEP-1999;
30-NOV-1999;
30-NOV-1999;
01-DEC-1999;
02-DEC-1999;
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08-MAR-1999;
02-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a novel human polypeptide. The specification describes novel polypeptides designated PRO201, PRO292, PRO327, PRO1265, PRO344, PRO343, PRO347, PRO357, PRO715, PRO117, PRO509, PRO853 and PRO882. These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumourigenesis. The polypeptides are useful target for the identification of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies against these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth
                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New anti-polypeptide antibody useful in the treatment neoplastic cell growth and proliferation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-452188/39.
N-PSDB; AAA46907.
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181
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                                                                                                                                                      APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                   APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
                                                                                                                                                                                                    MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
PFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
                 FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
                                                                 APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
                                                                                                                                   APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
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                                                                                                                                                                                                                                                                                                                                          243 AA;
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99WO-US20111.
99WO-US21090.
99WO-US28313.
99WO-US28301.
99WO-US28301.
99WO-US28565.
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99WO-US05028.
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68..74
/note=
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11..17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gurney
                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                      Score 243; DB 21;
Pred. No. 4.9e-212;
Pred. No. 6.9e-212;
Mismatches 0;
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Query Match
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Matches 243;
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16-DEC-1998;
22-DEC-1998;
                                                                                                                                                                                                                                                                            Baker KP,
Gerritsen N
Hillan KJ,
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PRO355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB01318 standard;
                                                                  New human nucleic acids encoding secreted and transmembrane polypeptides which are designated as PRO polypeptides are described polypeptides are described from membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources.
                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUN-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human
                                                                                                                                                                                             New human nucleic acids encoding polypeptides, designated as PRO pand diagnostic agents
                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200032776-A2
                                                                                                                                                                        Claim 12; Fig 18; 187pp;
                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       membrane
                                                                                                                                                                                                                                              2000-412324/35.
DB; AAA49560.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mbrane bound protein; secreted protein; PRO357; PRO327; PRO715; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347; PRO353; PRO361; PRO365; transmembrane polypeptide; y; screening; detection; inhibition; probe; primer; human.
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            Similarity .
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ME, Goddard A,
, Kljavin IJ, N
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100.0%;
llarity 100.0%;
Conservative 0;
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98US-0112850.
98US-0113296.
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216..222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "N-myristoylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
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A, Godowski
Napier MA,
                                                                                                                                                                           English
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 Score 243; DB 21;
Pred. No. 4.9e-212;
; Mismatches 0;
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i PJ, Grimaldi CJ, Gurn
, Roy MA, Tumas D, Woo
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02-DEC-1999

03-DEC-1999

16-DEC-1999

20-DEC-1999

20-DEC-1999
                                                                                                                                                                                                                                                                                                                                  Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
                                                                                                                                                                                                                                                              01-DEC-2000;
                                                                                                                                                                                                                                                                                 07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                Human PRO344 polypeptide sequence.
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                                                                                                                                                                                                                                                                                                                   Homo sapiens
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18-FEB-2000;
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                          2000WO-US00277.
2000WO-US00376.
2000WO-US03441.
2000WO-US04341.
2000WO-US04342.
2000WO-US04914.
2000WO-US05601.
2000WO-US05601.
2000WO-US05601.
2000WO-US07377.
2000WO-US07379.
2000WO-US0734944.
2000WO-US14042.
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99WO-US28634.
99WO-US28551.
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RESULT 9
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Best Local S
Matches 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrovytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCS), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerritsen Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO phlypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRO
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Human TANGO 253 SEQ ID NO:
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                                28-MAR-2001
                                                                    AAB65815;
                                                                                                    AAB65815 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptides, and to detect the presence of mammalian lung, colon, ast, prostate, rectal, cervical or liver tumours by comparing PRO
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                                                                                                                                                                                                                                                                                                                                            APIPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
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Stewart
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A, Godowski PJ, Gurney /
Tumas D, Watanabe CK, W
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Pred. No. 4.9e-212;
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y AL, Sherwood S;
Wood WI, Zhang Z
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences human and murine secreted or transmembrane proteins TANGO 253, 7 TANGO 281 and INTERCEPT 258. These are useful in the treatment coronary, pulmonary, olfactory, immunological, neurological, developmental and kidney disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acids for treating diseases and disorders, e.g atherosclerosis, infection, autoimmune diseases, obesity, disorders, brain disorders, tumors, diabetes, arthritis, sclerosis and asthma -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281; INTERCEPT 258; coronary disorder; olfactory disorder; neurological disorder; pulmonary disorder; immunological disorder; developmental disorder; kidney disorder.
                                          13-MAR-2001
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Human adipocyte complement related protein homolog zsig39.
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                                                                                                                    standard;
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Human; zacrp5; gene therapy;

complement inhibition; Clq domain;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC90045). ZACRP5 has a carboxyl-terminal C1q domain. The zacrp5 gene located on human chromosome 16. zacrp5 gene and protein are useful for diagnosing and treating inflammations, for determining arterial remodelling, for modulating calcium ion concentration, hormone secretion, DNA synthesis or cell growth, inositol phosphate turnover, arachidness to release the concentration of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel adipocyte complement related protein homolog, ZACRP5, useful for diagnosing and treating inflammation, vascular injury microbial
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Pred. No. 4.9e-212;
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RESULT 11 AAB49599

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FFGGWPKPASLSGGAMVRLBPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ

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                                                                                                                                                                                                                                                                                    protein homolog, ZACRP6 protein and coding sequence (see AAB49596 and AAC9051). ZACRP6 has a carboxyl-terminal Clq domain. The zacrp6 gene is located on human chromosome 21q. zacrp6 gene and protein are useful for diagnosing and treating inflammations, for determining arterial remodelling, for modulating calcium ion concentration, hormone secretion, DNA synthesis or cell growth, inositol phosphate turnover, arachidonate release, phospholipase C activation, gastric emptying, human neutrophil activation or ADCC capability and superoxide anion production. zacrp6 gene and protein are also useful as antimicrobial applications, preferably against bacteria and virus, for complement inhibition, for treating acute vascular injury, disseminated intravascular coagulation, arteriosclerosis and for wound healing. The present sequence is human adipocyte complement related protein homolog zsig39. This protein was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel adipocyte complement related protein homolog, ZACRP6, useful as modulators of neurotransmission and for treating disseminated intravascular coagulation, arteriosclerosis and acute vascular injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Piddington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammation; hormone secretion; inositol phosphate; arachidonate; phospholipase C activation; gastric emptying; neutrophil activation; superoxide anion production; antimicrobial; acute vascular injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; zacrp6; gene therapy; complement inhib adipocyte complement related protein homolog;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB49599;
                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-061532/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB49599 standard; Protein; 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ( OMYZ)
             121
                                                                                                                                                                            243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   healing;
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                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZYMOGENETICS
                                                                                                                                MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGRDGAPG
APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
                                              APGEKGEGGRPGLPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                              APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                               MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
                                                                                                                                                                                                                                                                        sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention
                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                           AA;
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                                                                                                                                                                                                                                                                          homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       relates to human adipocyte complement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    related protein homolog zsig39
                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                          comparison with ZACRP6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement inhibition; Clq domain;
                                                                                                                                                                                           Score 243; DB 22;
Pred. No. 4.9e-212;
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                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences of the human and murine secreted or transmembrane proteins TANGO 253, TANGO 27 TANGO 281 and INTERCEPT 258. These are useful in the treatment of coronary, pulmonary, olfactory, immunological, neurological, developmental and kidney disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acids for treating diseases and disorders, e.gatherosclerosis, infection, autoimmune diseases, obesity, disorders, brain disorders, tumors, diabetes, arthritis, sclerosis and asthma -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUN-2000; 2000WO-US16883
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                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 212-213; 332pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human mature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERCEPT
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                                                                                                           136
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                                                                                                                                                                                                                 SPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLPG
                                                                                                                                                                                                                                  SPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FFGGMPKPASLSGGAMVRLEPEDQVMVQVGVGDYIGIYASIKTDSTFSGFLVYSDMHSSP 240
                      MVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA
                                                                                            YDAVTGKFTCQVPGVYYPAVHATVYRASLQFDLVKNGESIASFFQFFGGWPKPASLSGGA
                                                                                                                                            PRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGH
                                                                                                                                                                   PRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGH
   MVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA
                                                                      YDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWPKPASLSGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McKay C,
                                                                                                                                                                                                                                                                                                                                                          228 AA;
                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coronary disorder; olfactory disorder;
isorder; pulmonary disorder; immunological disorder;
disorder; kidney disorder.
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                                                                                                                                                                                                                                                                              93.8%; 5c.
100.0%; Prr
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                                                                                                                                                                                                                                                                                    Score 228; DB 22; 1; Pred. No. 1.8e-198; 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diabetes, arthritis, multiple
                                                                                                                                                                                                                                                                                                                       Length 228;
                                                                                                                                                                                                                                                                                       Indels
   228
                                   243
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ABG12724
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Best Local
                                                                                                         Matches
                                                                                                                                                                            Sequence
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG12724 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biodiversity
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 85
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                                                                                                                          Similarity
   EAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFT 144
                                                                        PSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLPGPRGDPGPRG
                                     PSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLPGPRGDPGPRG
                                                                                                                                                                              220
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                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0540217.
2000US-0649167.
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                                                                                                                          100.0%;
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                                                                                                                          Score 213; DB 22;
Pred. No. 6.9e-185;
                                                                                                         Mismatches
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CC and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags are to restore normal activity of (II) is useful in gene therapy techniques (II). (II) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as (II) and its binding partners are useful in medical independent. (II) and its binding partners are useful for treating consisting of sites expressing (II). (I) and (II) are useful for treating consistency of the polypeptide and polynucleotide sequences have applications in the product of the polypeptide and polynucleotide sequences have applications in the produce other types of data and products dependent on DNA and CC diagnostics, forensics, gene mapping, identification of mutations consistency of the relations of the products of the polynucleotide sequences of the polynucleotide sequences of the polynucleotide sequences of data and products dependent on DNA and consistency of the polynucleotide sequences of data and products dependent on DNA and consistency of the polynucleotide sequences of the invention.

CC diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (TI) sequences. (PCR) primers, oligomers, and for chrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymerase chain reaction (PCR) primers, oligomers, and for cooling the polymerase chain reaction of (II). The and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
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o assess
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RESULT 14
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Best Local S
Matches 185
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                                                                                                                                                                                                                       The present invention provides the protein and coding sequences of the human and murine secreted or transmembrane proteins TANGO 253, TANGO 21 TANGO 281 and INTERCEPT 258. These are useful in the treatment of coronary, pulmonary, olfactory, immunological, neurological, developmental and kidney disorders.
                                                                                                                                                                                                                                                                                                                                      New nucleic acids for treating diseases and disorders, e.g. atherosclerosis, infection, autoimmune diseases, obesity, ear disorders, brain disorders, tumors, diabetes, arthritis, multiple
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                                                                                                                                                                                                 Sequence
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                                                            SDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASF 178
          FQFFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHS
                                                SDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASF
                                                                                                 PGAPGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPP
                                                                                                                 PGAPGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPP 118
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                                                                                                                                                                                        Sequence
                                                                                                                                                                                                               developmental and kidney disorders.
                                                                                                                                                                                                                           The present invention provides the protein and coding sequences human and murine secreted or transmembrane proteins TANGO 253, "TANGO 281 and INTERCEPT 258. These are useful in the treatment coronary, pulmonary, olfactory, immunological, neurological,
                                                                                                                                                                                                                                                                                       Disclosure; Page 274; 332pp; English.
                                                                                                                                                                                                                                                                                                                          New nucleic acids for treating diseases and disorders, e.g. atherosclerosis, infection, autoimmune diseases, obesity, ear disorders, brain disorders, tumors, diabetes, arthritis, multiple
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                                                             APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                              APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                              MRPLLVLLLLGLAAGS PPLDDNKI PSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
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llarity 100.0%;
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
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; Sequence 3, Application US/09336536
; Patent No. 6406884
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APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: McKay, C.
APPLICANT: McKay, C.
APPLICANT: BOSSONE, S.
FILE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOPTMARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 243
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US-09-336-536-4
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CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
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APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
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Matches 243; Conserv
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ORGANISM: Homo sapiens
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  PRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGH
                    PRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGH 135
                                                                              SPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGEKGEGGRPGLPG 60
                                                                                                   SPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLPG 75
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                                                                                                                                                                                            Length 228;
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US-09-336-536-7
Query Match
Best Local Similarity
Thes 70; Conserva
                                                                                                                                                                                                        APPLICANT: Sleeman, Matthew
APPLICANT: Orrust, Rene
APPLICANT: Orrust, Rene
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Sk:
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-188-930-295
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                                                                                              ; TYPE: PRT
; ORGANISM: Rat
US-09-188-930-295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 7
                                                                                                                                                  SOFTWARE: FASUSEQ for Windows Version 3.0 SEQ ID NO 295
LENGTH: 243
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Best Local (
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CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Leiby, K.
APPLICANT: MCKBY, C.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND
PILE REFERENCE: 7853-144
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Watson, James D. APPLICANT: Strachan, Lorna APPLICANT: Sleeman, Matthew APPLICANT: Onrust, Rene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver.
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 YDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWPKPASLSGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 YDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWPKPASLSGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 AFSAKRSESRVPPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128;
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>. 6406884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASL
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                    ilarity 100.0%; I Conservative 0;
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100.0%; Pred. No. 9.7e-112;
                                        28.8%; Score 70; 100.0%; Pred. No.
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                                                          DB 4;
                                        1.6e-57;
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                                                        Length 243;
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Mismatches

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; LENGTH: 243
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-336-536-10
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US-09-336-536-10
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-336-536-11
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                                                                                                                                                            Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Leiby, K.
APPLICANT: MCKBY, C.
APPLICANT: BOSSOME, S.
APPLICANT: BOSSOME, S.
APPLICANT: BOSSOME, S.
TITLB OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 199-06-18
NUMBER OF SEQ ID NOS: 75
NUMBER OF SEQ ID NOS: 75
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES
FILE REFERENCE: 7853-144
                                                                                                                                                          Local
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                                                                 182 FGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSPV 241
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242 FA 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62;
                                                                                                                                           62; Conserv
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                               FA 243
                                                                                                     FGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSPV 241
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                                                                                                                                       25.5%; Score 62; DB 4; Lilarity 100.0%; Pred. No. 4.5e-50; Conservative 0; Mismatches 0;
                                                                                                                                                                           Length 243;
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                                                                                                                                           Indels
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RESULT 10
US-09-336-536-13
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                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
SOPTWARE: PATENTIN VEY: 2.0
SEQ ID NO 14
LENGTH: 128
                                                                                                                                                              Matches
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Best Local Similarity 100.0%; Pred. No. 9.6e-49;
Matches 60; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 6
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APPLICANT: McKay, C.
APPLICANT: Bossone, S.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES
FILE REFERENCE: 7853-144
                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Heiby, K.
APPLICANT: MCKAY, C.
APPLICANT: BOSSONE, S.
APPLICANT: BOSSONE, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 7853-144
                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                      182 FGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLV 232
                                                                                 78
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                                                                                                                                                              51;
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                                                                                                                                                              Conservative
                                                                                                                                                                              21.0%; Score 51; DB 4; Length 128; 100.0%; Pred. No. 4.4e-40;
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                                                                                                                                                            Mismatches
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Sequence 13, Application US/09336536 Patent No. 6406884

GENERAL INFORMATION:

CURRENT APPLICATION NUMBER: US/09/336,536 CURRENT FILING DATE: 1999-06-18 NUMBER OF SEQ ID NOS: 75

APPLICANT: Leiby, K.
APPLICANT: MCKAY, C.
APPLICANT: Bossone, S.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-144

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US-09-336-536-5
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US-09-227-357-190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-336-536-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT ; ORGANISM: Mus musculus US-09-336-536-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 17.7
Best Local Similarity 100.
Matches 43; Conservative
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Patent No. 63425
                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 7853-144
CURRENT APPLICATION NUMBER: US/09/336,536
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Leiby, K.
APPLICANT: McKay, C.
APPLICANT: Bossone, S.
APPLICANT: BOSSONE, SECRETED PROTEINS AND USES THEREOF
                                                                                          EARLIER
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                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 1999-01-08
                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/227,357
                                                                                                                                                                                                                                                                                                       FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                             3ARLIER
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                                                                                                                                                                                                                      APPLICATION NUMBER: 60/051,926
                                                                                                                                                                       APPLICATION NUMBER: 60/052,793 FILING DATE: 1997-07-08
                                                            APPLICATION NUMBER: 60/052,732
                                                                                                             FILING DATE: 1997-07-08
                                                                                                                                                        APPLICATION NUMBER: 60/051,925
APPLICATION NUMBER: 60/051,932
                              APPLICATION NUMBER: 60/051,931
                                               FILING DATE:
                                                                                          APPLICATION NUMBER: 60/052,803
                                                                                                                          APPLICATION NUMBER: 60/051,929
                                                                                                                                           FILING DATE: 1997-07-08
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                                                                              FILING DATE: 1997-07-08
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                                                                                                                                                                                                           LING DATE:
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                                               1997-07-08
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100.0%; Pred. No.
tive 0; Mismatc
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Pred. No.
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                                                                                                           ; LOCATION: (128)
; OTHER INFORMATION:
US-09-227-357-190
                                Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 190
LENGTH: 128
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EARLIER
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                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 672
                                                                                                                                                                                                                                                                                                                                                                                      EARLIER FILING DATE: 1997-09-12
                                                                                                                                                                                                    LOCATION: (127)
OTHER INFORMATION:
                                                                                                                                                                 NAME/KEY: SITE
                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/058,660
45 GLPGRDGRDGR 55
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APPLICATION NUMBER: 60/055,964
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APPLICATION NUMBER: 60/052,733
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PILING DATE: 1997-07-08
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                                    ilarity 100.0%;
Conservative (
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                                    0;
                                                       Score 11; ; Pred. No.
                                      Mismatches
                                                                                                                                                                                                    of the naturally occurring L-amino acids
                                                     DB 4;
0.0074;
                                                                       Length 128;
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US-08-931-820-4

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Patent No.
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino aci
       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MCOMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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HYPOTHETICAL: NO
ORIGINAL SOURCE:
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PRIOR APPLICATION DATA:
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ADDRESSEE: Darby & I
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                           CITLE OF INVENTION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                 STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
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APPLICATION NUMBER:
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5. 6110689
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Bonde, Martin
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Method and Use of the Method to Diagnose the Presence
Disorders Associated with the Metabolism of
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                                                                                                                                                                                                                                                                                                         A Method for Assaying Collagen Fragments
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/note= "Ala may be Pro"
US/08/963,825
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Pred. No.
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US-09-500-811-21
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
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ATTORNEY/AGENT INFORMATION:
NAME: GOGODIS, Adda C
REGISTRATION NUMBER: 29,714
                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Qvist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Met
TITLE OF INVENTION: in Bo
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                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER:
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CORRESPONDENCE ADDRESS:
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                                             TELECOMMUNICATION INFORMATION:
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les 10; Conservative (
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TELEPHONE: 212-753-6237
                                                                               NAME: Gogoris, Adda C
REGISTRATION NUMBER:
                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                    FILING DATE
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                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                               805 Third Avenue
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                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                               York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Method for Assaying Collagen Fragments
A Method for Assaying Collagen Fragments
in Body Fluids, A Test Kit and Means for Carrying Out the
Method and Use of the Method to Diagnose the Presence of
Method and Use of the Method to Diagnose the Presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.1%; Score 10; DB 3
100.0%; Pred. No. 0.4;
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                                                                 4305/08701
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INPORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
INMEDIATE SOURCE:
COLLAGEN ALPHA 1 (III)
US-09-500|811-21

Query Match
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps
Oy 60 GAPGEKGEGG 69

Qy 60 GAPGEKGEGG 690

Search completed: June 20, 2003, 11:44:09
Job time: 21 secs
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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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Copyright (c) 1993 - 2003 Compus
/cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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243	243	6.57	2	243	243	243	243	243	243	243	243	243	243	243	243	243	243	243	243	Score
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243	243	647	242	243	243	243	243	243	243	243	243	243	243	243	243	243	243	243	243	Length DB
9 US-10-140-002-362	9 US-10-143-114-362	A 00-T0-T47-707-007	0 110-10-140-431-360	9 US-10-140-474-362	9 US-10-137-865-362	9 US-10-176-921-362	9 US-10-176-918-362	9 US-10-175-746-362	9 US-09-796-753-68	9 US-10-140-470-362	9 US-10-123-904-362	9 US-10-121-049-362	9 US-10-028-072-362	9 US-09-944-929-42	9 US-09-944-907-42	9. US-09-944-944-42	9 US-09-944-896-42	9 US-09-944-403-42	9 US-09-944-413-42	BID
Sequence 362, App			27				Sequence 362, App				Sequence 362, App				-	Sequence 42, Appl	-	•	Sequence 42, Appl	Description

45	44	43	42	41	40	39	38	37	36	35	34	<u>კ</u>	32	31	30	29	28	27	26	25	24	23	22	21	20
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US-10-123-909-362	US-10-123-908-362	US-10-123-902-362	US-10-123-215-362	US-10-121-047-362	US-10-121-043-362	US-10-121-041-362	US-09-944-884-42	US-10-160-498-362	US-10-140-925-362	US-10-124-822-362	US-10-124-819-362	US-10-123-903-362	US-10-123-292-362	US-10-121-045-362	US-10-140-928-362	US-10-140-921-362	US-10-123-261-362	US-10-123-236-362	US-10-123-108-362	US-10-143-032-362	US-10-141-755-362	US-10-121-050-362	US-10-142-423-362	US-10-123-262-362	US-10-142-419-362
	Sequence 362, App	•		Sequence 362, App				•				Sequence 362, App			Sequence 362, App			Sequence 362, App		•	-	•	•	Sequence 362, App	•

ALIGNMENTS

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US-09-944-413-42
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                                                                                                   PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR APPLICATION NUMBER: 60/069,425
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APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/944,413
CURRENT FILING DATE: 2001-09-26
CRICK APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR FILING DATE: December 3, 1997
                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1
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                                    PRIOR APPLICATION NUMBER: 60/069, PRIOR FILING DATE: December 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                     PRIOR FILING DATE: December 12,
FILING DATE:
                       APPLICATION NUMBER: 60/069,
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US20020156004A1
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Tumas, Daniel
Wood, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Napier, Mary
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Kljavin, Ivar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gurney, Austin
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Grimaldi, Christopher
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December 16,
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APPLICATION NUMBER: 60/068,

APPLICATION NUMBER: 60/069

60/069

December

APPLICATION NUMBER:

60/069,702

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/944,403
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR FILING DATE: December 3, 1997
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APPLICANT:
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PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                 FILING DATE: December 17, 1
APPLICATION NUMBER: 60/068,
FILING DATE: December 18, 1
                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/069,694 FILING DATE: December 16, 1997
                                                                                                                                                                                                                APPLICATION NUMBER: 60/069,702 FILING DATE: December 16, 1997
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                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/069,425
                                                                                                                                                  APPLICATION NUMBER: 60/069,873
                                                                                                                                                                                                             FILING DATE:
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FILING DATE:
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                                                                 APPLICATION
                                                                                                                                                                    FILING DATE:
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Goddard, Audrey
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Roy, Margaret
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Grimaldi,Christopher
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Filvaroff, Ellen
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                                                                 NUMBER: 60/070,
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US-09-944-403-42
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SEQ ID NO 42
LENGTH: 243
TYPE: PRT
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Best Local Similarity
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FILING DATE: June 22, 1999
APPLICATION NUMBER: PCT/US99/21090
FILING DATE: September 15
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APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020165143A1ember 30, 1999
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APPLICATION NUMBER: PCT/US00/04414
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APPLICATION NUMBER: PCT/US99/30095
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APPLICATION NUMBER: PCT/US99/28409
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APPLICATION NUMBER: 09/218,517
FILING DATE: December 22, 1998
APPLICATION NUMBER: 09/216,021
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                                                                          APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
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RESULT 3
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PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: P2548D1C1
CURRENT APPLICATION NUMBER: US/09/944,896
CURRENT FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                 FILING DATE: APPLICATION
                                                                                                                           APPLICATION NUMBER: 60/075,945
FILING DATE: February 25, 1998
APPLICATION NUMBER: 60/112,850
                                                                APPLICATION NUMBER: 60/146,222
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FILING DATE: December 11, 1997
APPLICATION NUMBER: 60/069,278
FILING DATE: December 11, 1997
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                                                                                            APPLICATION NUMBER: 60/113,296
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Grimaldi, Christopher
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NUMBER: 60/069,
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                 July 28, 1999
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NIMBER: PCT/US98/19330
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RESULT 4
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SEQ ID NO 42
LENGTH: 243
Sequence 42, Application US/09944944
Patent No. US20020173463A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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Best Local Similarity
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PRIOR FILING DATE: Pebruary 28
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TYPE: PRT
ORGANISM: Homo Sapien
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APPLICATION NUMBER: 09/2...
APPLICATION NUMBER: 09/2...
TYPING DATE: March 3, 1999
TYPING DATE: MARCH 3, 1999/12252
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APPLICATION NUMBER: PCT/US00/32678
FILING DATE: December 1, 2000
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APPLICATION NUMBER: PCT/US00/04414
FILING DATE: February 22, 2000
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APPLICATION NUMBER: PCT/US99/30095
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APPLICATION NUMBER: PCT/US99/28409
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APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: PCT/US00/20710
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Pred. No. 7.9e-202;
D; Mismatches 0;
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                                                             APPLICATION NUMBER: FILING DATE: June 22,
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APPLICATION NUMBER: PCT/US99/28409
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N NUMBER: 09/216,021
S: December 16, 1998
N NUMBER: 09/218,517
E: December 22, 1998
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NUMBER: 60/075,
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US-09-944-944-42
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SEQ ID NO 42
LENGTH: 243
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Best Local Similarity
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OR APPLICATION NUMBER: PCT/US00/05841
OR HILING DATE: March 2, 2000
OR APPLICATION NUMBER: PCT/US00/08439
OR FILING DATE: March 30, 2000
OR APPLICATION NUMBER: PCT/US00/14042
OR FILING DATE: May 22, 2000
OR APPLICATION NUMBER: PCT/US00/20710
OR APPLICATION NUMBER: PCT/US00/20710
OR APPLICATION NUMBER: PCT/US00/32678
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FILING DATE: No. US20020173463Alember
APPLICATION NUMBER: PCT/US99/28301
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APPLICATION NUMBER: PCT/US00/04414
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Botstein, David
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                                                Gurney, Austin
Hillan, Kenneth
                                                                                    Godowski, Paul
Grimaldi, Christopher
                                                                                                                        Gerritsen, Mary
Goddard, Audrey
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Roy, Margaret
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Pred. No. 7.9e-202;
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FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,929
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 42
LENGTH: 243
TYPE: PRT
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SEQ ID NO 42
LENGTH: 243
TYPE: PRT
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Best Local :
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PRIOR APPLICATION NUMBER: 09/866,028
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                                                                                                                                                                         Roy, Margaret
Tumas, Daniel
Wood, William
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Hillan, Kenneth
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Godowski, Paul
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PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059117
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059263
PRIOR APPLICATION NUMBER: 60/059263
PRIOR PILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR PILING DATE: 1997-09-19
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CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
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US-09-944-929-42
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Best Local Similarity
Matches 243; Conserv
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Publication No
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TITLE OF INVENT:
FILE REFERENCE:
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INVENTION:
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Gao, Wei-Qiang
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Wood, William
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                                                                                                                                                                                                                                                                                                                                                                                 Tumas,Daniel
                                                                                                                                                                                                                                                                                                                                                                                                             Smith, Victoria
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APPLICATION NUMBER: 60/063329
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APPLICATION NUMBER: 60/085579
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APPLICATION NUMBER: 60/088741
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                           CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File
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DR FILING DATE: 1998-07-01
DR APPLICATION NUMBER: 60/091519
DR FILING DATE: 1998-07-02
DR APPLICATION NUMBER: 60/091982
DR FILING DATE: 1998-07-07
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APPLICATION NUMBER: 60/
FILING DATE: 1998-06-26
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Watanabe, Colin K
Wood, William
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 362
LENGTH: 243
TYPE: PRI
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Best Local Similarity
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P333ORIC54
CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
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APLPPDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
                                                                     APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD 120
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Watanabe, Colin K
Wood, William
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100.0%; Pred. No. 7.9e-202;
tive 0; Mismatches 0;
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; NUMBER OF SEQ ID NOS: 55
; SEQ ID NO 362
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-470-362
RESULT 11
US-09-796-753-68
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US-10-140-470-362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
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TITLE OP INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OP INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330R1C160
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                                                                VFA 243
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Gerritsen, Mary E.
Goddard, Audrey
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DeForge, Laura
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NOS: 550
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                                                                                            ; TYPE: PRT
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US-09-796-753-68
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Best Local Similarity
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Publication No. US20030027998A1
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PRIOR APPLICATION NUMBER: 09/183,175
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                                                                                                                                                ID NO 68
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APPLICATION NUMBER: 09/342,687
FILING DATE: 1999-06-29
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APPLICATION ,NUMBER:
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APPLICATION NUMBER:
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APPLICATION NUMBER: 09/516,745
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WENTION: SECRETED PROTEINS AND USES
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llarity 100.0%;
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JMBER: 09/665,666
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Pred. No. 7.9e-202;
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NUMBER OF SEQ ID NO:
SEQ ID NO 362
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sap:
US-10-175-746-362
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                   FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP 240
                                                     VFA 243
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Filvaroff, Ellen
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R1C353
CURRENT APPLICATION NUMBER: US/10/175,746
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                                                                                                                                                                                         Local Similarity 100.0%; es 243; Conservative 0
                           APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAPSAKRSESRVPPPSD 120
                                                                                                                             MRPLLVLLLGLAAGS PPLDDNKI PSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGRDGAPG
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Pred. No. 7.9e-202;
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RESULT 13
US-10-176-918-362
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Best Local Similarity 100.0%;
Matches 243; Conservative (
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 362
LENGTH: 243
                             Sequence 362, Application US/10176921 Publication No. US20030027276A1 GENERAL INFORMATION:
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 APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maur
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TYPE: PRT
ORGANISM: Homo Sapien
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Watanabe, Colin K
Wood, William
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Godowski, Paul J.
Gurney, Austin L.
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Beresini, Maureen
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Pred. No. 7.9e-202;
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RESULT 15
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US-10-176-921-362
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 362
LENGTH: 243
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Best Local Similarity
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CURRENT FILING DATE: 2002-06-20
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C288
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100.0%; Pred. No. 7.9e-202;
tive 0; Mismatches 0;
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APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: PPLICANT: PPLICANT Baker, Kevin Beresini, Maureen DeForge, Laura Smith, Victoria Sherwood, Steven Gurney, Austin L. Goddard, Audrey Godowski, Paul J. Gerritsen, Mary E. Gao, Wei-Qiang Desnoyers, Luc Filvaroff, Ellen Tumas,Daniel Stewart, Timothy A ۳.

GENERAL INFORMATION: Sequence 362, Ap

Application US/10137865 o. US20030032155A1

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SEQ ID NO 362
LENGTH: 243
TYPE HPRT
ORGANISM: Homo Sapien
US-10-137-865-362
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Search completed: June 20, 2003, 11:47:19 Job time : 24 secs
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLBIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C154
CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT FILING DATE: 2002-05-03
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181 PFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP 240
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CAP18 precursor -	antibacterial pept	hypothetical prote	conserved hypothet	probable integral	hypothetical prote	hypothetical prote	collagen alpha 1	hypothetical prote	collagen alpha	collagen alpha	translation init	collagen alpha 2	amyloid precursor-	beta-amyloid precu	collagen alpha j

ALIGNMENTS

RESULT 2 T34241 Typotheri C;Species C;Accessi R;Wilson, submitted A;Descrip A;Referen A;Accessi A;Status:	dg Qg	B 8	B &	Db Qy	Query M Best Lo Matches	C;Genetics: A;Note: DKF C;Superfami	A; Molecule A; Residues A; Cross-re A; Experime	R;Ottenwa submitted A;Referen A;Accessi A;Status:	RESULT 1 T14782 hypothetic C;Species: C;Date: 20 C;Accessio
RESULT 2 T34241 T34241 T34241 Typothetical protein F26F12.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000 C;Accession: T34241 R;Wilson, R.; Bentley, D.; Gattung, S. submitted to the RMEL Data Library, April 1996 A;Bescription: The sequence of C. elegans cosmid F26F12. A;Reference number: Z21493 A;Accession: T34241 A;Status: preliminary; translated from GB/EMBL/DDBJ	205 VMVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA 243 	145 CQVPGVYYPAVHATVYRASLQFDLVKNGESIASFFQFFGGWPKPASLSGGAMVRLEPEDQ 204 	85 EAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFT 144 	25 PSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLPGPRGDPGPRG 84	Query Match 90.1%; Score 219; DB 2; Length 219; Best Local Similarity 100.0%; Pred. No. 1.5e-199; Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	ics: DKFZp586B0621.1 family: complement Clq carboxyl-tern	A;Molecule type: mRNA A;Residues: 1-219 <0TT- A;Cross-references: EMBL:AL110261 A;Experimental source: adult uterus; clone DKFZp586B0621	R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, August 1999 A;Reference number: Z18184 A;Accession: T14782 A;Actession: T14782 A;Actession: T24782 A;Actes preliminary	T14782 T14782 hypothetical protein DKF2p586B0621.1 - human (fragment) C;Species: Homo sapiens (man) C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Sep-2000 C;Dates: 174782

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surfactant protein D - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 02-Dec-1993 #sequence_revision 01-
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C; Superfamily:
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A;Title: Primary structure of rat pulmonary surfactant protein D. A;Reference number: A42046; MUID:92112913; PMID:1370483
A;Accession: A42046
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C;Species: Rattus norvegicus (Norway rat)
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A; Residues: 1-369 <LIM>
C; Superfamily: pulmonary
F; 248-367/Domain: C-type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Lim, B.L.; Lu, J.; Reid, K.B.M. Immunology 78, 159-165, 1993
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A;Experimental source: strain Bristol N2; clone F26F12
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A; Residues: 1-289 < WIL>
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A;Experimental source: lung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H.; Pisher, J.H.; Papst, P.; Benson, B.; Lau, K.; Mason, R.J.; Voelker, D.R.
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C;Species: Homo sapiens (man)
C;Jate: 16-Apr-1999 #sequence revision 16-Apr-1999 #text_change 22-Jun-1999
C;Accession: A45225; S23434; S24555; S44420; S18382; A56776
R;Crouch, E.; Rust, K.; Veile, R.; Donis-Keller, H.; Grosso, L.
J. Biol. Chem. 268, 2976-2983, 1993
A;Title: Genomic organization of human surfactant protein D (SP-D). SP-D is A;Reference number: A45225; MUID:93155122; PMID:8428971
A;Accession: A45225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Accumulation of surfactant protein D in human pulmonary alveolar proteinosis A;Reference number: A56776; MUID:93142849; PMID:8424457 A;Accession: A56776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Rust, K.; Grosso, L.; Zhang, V.; Chang, D.; Persson, A.;
Arch. Biochem. Biophys. 290, 116-126, 1991
A;Title: Human surfactant protein D: SP-D contains a C-type
A;Reference number: S18382; MUID:91378578; PMID:1898081
A;Accession: S18382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Hoppe, H.J.; Barlow, P.N.; Reid, K.B.M.
FEBS Lett. 344, 191-195, 1994
A;Title: A parallel three stranded alpha-helical bundle
A;Reference number: S44420; MUID:94244769; PMID:8187882
A;Accession: S44420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pulmonary surfactant
F;46-222/Domain: collagenous #status predicted <COL>F;223-375/Domain: non-collagenous #status predicted <NC2>F;223-375/Domain: C-type lectin homology <CGH>F;254-373/Domain: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                     A;Map position: 10q22.2-10q23.1
C;Superfamily: pulmonary surfactant protein D; C-type lectin homology
C;Superfamily: pulmonary surfactant protein D; C-type lectin homology
C;Kepwords: blocked amino end; calcium; glycoprotein; hydroxylysine; hydroxyproline;
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-375/Product: pulmonary surfactant protein D #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Experimental source: bronchoalveolar lavage
A;Experimental source: bronchoalveolar lavage
A;Note: sequence extracted from NCBI backbone (NCBIP:123024, NCBIP:123023); sequence
C;Comment: Pulmonary surfactant is a complex of phospholipids and proteins that lower
C;Comment: This protein is synthesized by alveolar type II cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 46-58, 'F', 60-
                                                                                                                                                                                                                                                                                                                                                          A;Gene: GDB:SFTPD; SFTP4; SP-D
A;Cross-references: GDB:132674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 46-58,'F',60-62,'E',64-72;223-227,'X',229-239,'P',241-245,'X',247-256,'X'
A;Cross_references: PIDN:AAB25037.1; PID:9263973; PIDN:AAB25038.1; PID:9263974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Crouch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 'F',60-205,'P',207-374,'HF' <RUS>
A;Cross-references: GB:L05485; NID:g292505
                                                                                                                                           F;21-45/Domain: non-collagenous #status predicted <NCl>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Lu, J.; Willis, A.C.; Reid,
iochem. J. 284, 795-802, 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Residues: 214-234,'X',236,'XX',239-241 <LUJ2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: S24555;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B.; Persson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202-257 <HOP>
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   (covalent) #status predicted
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A;Molecule type: mRNA
A;Residues: 1453-1593, A',1595-1670 <MOR>
A;Cross-references: GB:S55790; NID:g234418; PIDN:AAB19637.1;
C;Comment: Prolines and lysines at the third position of the
ed and subsequently O-glycosylated.
                                                                                                                                                                                                                                   R;Morrison, K.B.; Mariyama, M.; Yang-Feng, T.L.; Reeders, S.T. Am. J. Hum. Genet. 49, 545-554, 1991
A;Title: Sequence and localization of a partial cDNA encoding A;Reference number: A39786; MUID:91353570; PMID:1882840
A;Accession: A39786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Contents: annotation; erratum; correction to intronic s R;Bernal, D.; Quinones, S.; Saus, J.
J. Biol. Chem. 268, 12090-12094, 1993
A;Title: The human mENA encoding the Goodpasture antigen A;Reference number: A45971; MUID:93280184; PMID:8505332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M92993; NID:g177895; PIDN:AAA21610.1; PID:g177896
A;Note: sequence extracted from NCBI backbone (NCBIP:115597)
R;Quinones, S.; Bernal, D.; Garcia-Sogo, M.; Elena, S.F.; Saus, J.
J. Biol. Chem. 269, 17358, 1994
A;Reference number: #44738; MUID:94274734; PMID:8006044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Turner, N.; Mason, P.J.; Brown, R.; Fox, M.; Povey, S.; Rees, A.; Pusey, C.D. J. Clin. Invest. 89, 592-601, 1992
A;Title: Molecular cloning of the human Goodpasture antigen demonstrates it to A;Reference number: A43928; MUID:92147878; PMID:1737849
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: nucleic acid sequence not shown
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A;Accession: A44043
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A;Experimental source: kidney
R;Quinones, S.; Bernal, D.; Garci
J._Biol._Chem., 267, 19780-19784,
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A;Cross-references: GB:X80031; NID:g577563; PID:g577564
A;Experimental source: kidney
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C;Species: Homo sapiens (man)
C;Date: 28-Oct 1994 #sequence revision (
C;Accession: A54763; A49208; Ā44043; A45
C;Accession: A54763; A49208; Ā44043; A45
R;Mariyama, M.; Leinonen, A.; Mochizuki
J. Biol. Chem. 269, 23013-23017, 1994
                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1427-1444 <BER>
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A; Residues: 1331-1524, 'I', 1526-1670 < TUR>
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                                                                                Comment: In Goodpasture's
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Accession: A54763; A43928; A44043; A45971; A39786
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Biol. Chem. 269, 23013-23017, 1994
                                                                                                                                                                                                                                                                                                                                 sequence extracted from NCBI backbone (NCBIP:133363); sequence son, K.E.; Mariyama, M.; Yang-Feng, T.L.; Reeders, S.T.
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GDB:128351;
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                                                                             syndrome,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garcia-Sogo, M.; Elena,
1784, 1992
OMIM:120070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
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                                                                          an autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tryggvason, K.; Reeders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intronic sequence
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                                                                       response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is alternatively spliced
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                                                                  develops against an epitop
                                                                                                                       tripeptide repeating
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A;Introns: 1385/1; 1418/1; 1488/1; 1547/2; 1585/3; 1643/2 #status incomplete A;Note: the alpha 3(IV) and alpha 4(IV) chain genes are encoded on opposite strate; C;Complex: This minor type IV collagen is thought to form a heterotrimer of two mong trimer amino-terminal domains (with disulfide and desmosine cross-links), deer associations in the interrupted helical domain (with disulfide and desmosine
                                                                                                                                                                                                                                                                F;1460-1548,1493-1551/Disulfide bonds: F;1505-1511,1616-1622/Disulfide bonds:
                                                                                                                                                                                                                                                                                                                          F:1345-1347/Region: cell attachment (R.G.D) motif
F;1437-1434/Region: cell attachment (R.G.D) motif
F;1439-1670/Domain: celloxyl-terminal nonhelical, NC1 <NC1>
F;1451-1551/Domain: collagen IV carboxyl-terminal repeat <CT1>
F;1451-1551/Domain: collagen IV carboxyl-terminal repeat <CT2>
F;1561-1665/Domain: collagen IV carboxyl-terminal repeat <CT2>
F;1561-1665/Domain: collagen IV carboxyl-terminal repeat <CT2>
F;353,33,39,41,125,422,476,479,682,722,809,1387/Disulfide bonds: interchain #status
F;353/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                   F;1570-1662,1604-1665/Disulfide bonds:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;1306-1308/Region: cell attachment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;1154-1156/Region: cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 2q36-2q37
                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superfamily: collagen alpha 1(IV) chain

Keywords: alternative splicing; basement membrane; cell binding; coiled coil; extr.

1-28/Domain: signal sequence #status predicted <SIG>
1/29-1670/Product: collagen alpha 3(IV) chain, long splice form #status predicted <NO.
                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    791-793/Region: cell attachment (R-G-D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43-1438/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-42/Domain: amino-terminal nonhelical, NH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description: minor structural component of extracellular
1300
                                                      71
                                                                                                                                                Similarity
                                                         PGLPGPRGDPG
                                                                                                                   Conservative
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                                                                                                                                         Pred. No. 0.074;
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                                                                                                                                                                                                                                #status predicted (or 1570-1665, 16
                                                                                                                                                                                                                                                                                             (covalent) #status predic
(or 1460-1551, 1493-1548)
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C;Date: 04-Nov-1994 #sequence revision 04-Nov-1994 #text change C;Accession: A5849; PH0844; S16316; I56328; A30296; I84686 R;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J. J. Biol. Chem. 269, 20256-20262, 1994 A;Title: Cloning of human type VII collagen. Complete primary se A;Reference number: A54849; MUID:94327588; PMID:8051117 A;Accession: A54849 A; Molecule type: mRNA A; Residues: 1-2944 <C N;Alternate collagen alpha 1(VII) chain precursor -Status: not compared with conceptual translation Species: Homo 1-2944 <CHR> names: procollagen alpha 1(VII) chain sapiens (man) sequence of the alphal 20-Sep-1999

A;Cross-references: GB:L02870; NID:g987124; PIDN:AAA75438.1; PID:g987125
R;Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S.

R;Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S. Biochem. Biophys. Res. Commun. 183, 958-963, 1992 A;Title: Molecular cloning and characterization of type A;Reference number: PH0844; MUID:92231902; PMID:1567409 A;Accession: PH0844

VII collagen

A;Molecule type: mRNA
A;Residues: 'EFR',340-475,'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG',524-528,
A;Cross-references: DDBJ:D11152; DDBJ:D13694; NID:g453698; PIDN:BAA02853.1; PID:g45:
A;Experimental source: keratinocyte

A;Note: the authors translated the codon ACC for residues 3: R;Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A;Title: Human type VII collagen: cDNA cloning and chromoson A;Reference number: S16316; MUID:91334380; PMID:1871109
A;Accession: S16316. 394 and Wynn,

ning and chromosomal PMID:1871109 mapping

of the

A; Molecule type: mRNA

A;Residues: 815-892,'E',894-1439 <PAR>A;Cross-references: GB:M65158; GB:S490
A;Experimental source: keratinocyte :M65158; GB:S49017; keratinocyte NID:g180914; PIDN:AAA96439.1; PID:g180915

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F;231-318/Domain: fibronectin type III re F;327-413/Domain: fibronectin type III re F;327-413/Domain: fibronectin type III re F;414-52/Domain: fibronectin type III re F;508-593/Domain: fibronectin type III re F;598-683/Domain: fibronectin type III re F;686-771/Domain: fibronectin type III re F;776-862/Domain: fibronectin type III re F;776-952/Domain: fibronectin type III re F;684-952/Domain: fibronectin type III re
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A;Title: The carboxyl-terminal half of type VII collagen, A;Reference number: 148103; MUID:93271985; PMID:8499916
A;Accession: 184686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:L06862; NID:g388713; PIDN:AAA89196.1; PID:g388714
R;Christiano, A.M.; Ryynaenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-353, 1994
A;Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly A;Reference number: A55255; MUID:94224777; PMID:8170945
A;Contents: annotation
F;2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
F;2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F;337,786,1199/Binding site: carbohydrate (Asn) (covalent) #status predicte
F;2167,2176,2185,2188,2664,2667,2673/Modified site: 4-hydroxyproline (Pro)
F;2625,2631/Modified site: 5-hydroxylysine (Lys) #status experimental
F;2625,2631/Binding site: carbohydrate (Lys) (covalent) #status experimental
F;2634,2802,2804/Disulfide bonds: interchain #status predicted
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A; Residues: 'EFR',372-517,'DV',520-540,'W',542-1255 <RES>
A; Cross-references: GB:S51236; NID:g262308; PIDN:AAB24637.1; PID:g262309;
R; Seltzer J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.;
J. Biol. Chem. 264, 3822-3826, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion protA;Reference number: I56328; MUID:93107742; PMID:1469284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Gammon, W.R.;
J. Invest. Derma
                                                                                                                                                                                                                                                                                                                                                                                   F;954-1045/Domain: fibronectin type III rep. F;1052-1219/Domain: von Willebrand factor t; F;1170-1172/Region: cell attachment (R-G-D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;17-1253/Domain: amino-terminal nonhelical #status predicted F;36-201/Domain: von Willebrand factor type A repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: GDB:COL7A1; EBR1; EBD1; EB
A;Cross-references: GDB:128750; OMIM:120120
A;Map position: 3p21.3-3p21.3
A;Note: defects in this gene can result in dominant and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 'A',1240-1246,'G',1248-1250,'XE',1253-1255,'Q',1257,'E';2032,'C',2034-2041;
A;Note: two reported peptides cannot be reliably located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem. 264, 3822-3826, 1989
A; Title: Cleavage of type VII collagen by interstitial collagenase and type IV A; Reference number: A30296; MUID:89139437; PMID:2537292
                                                                                                                                                                                                                                                                                                                        F;1189-1253/Region:
F;1254-2783/Region:
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A;Residues: 2395-2871,'S',2873-2944 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description: structural component of extracellular polymer associated with anchoring Superfamily: unassigned collagens; animal Kunitz-type proteinase inhibitor homology; Keywords: colled coll; extracellular matrix; glycoprotein; hydroxylysine; hydroxypro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
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                                                                                                                                                                                                                               ;2008-2010/Region:
;2553-2555/Region:
                                                                                                                                                                                                                                                                                              ;1334-1336/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complex: type VII collagen is probably a homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Comment: Prolines and lysines at the third position of and subsequently O-glycosylated.
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                                                                                                                                                                                                                               cell attachment (R-G-D) cell attachment (R-G-D)
                                                                                                                                                                                                                                                                                                                        cysteine/proline-rich interrupted helical
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III repeat homology
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                                          (covalent) #status experimental
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GLPGRDGRDG 54

Matches Query Match Best Local

Similarity

4.1%; . 0%;

Score 10; ; Pred. No.

DB 1; 0.13;

Length 247

0,

Gaps

0

. No.

Conservative

0

;206/Binding site: carbohydrate (Asn) (covalent) ;126-245/Domain: C-type lectin homology <LCH>

amino end

(Ser)

(in mature #status

predicted

form) #status predicted

16/Modified site: acetylated

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39 5

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R;Shamansky, L.M.; Pratt, D.; Boisvenue, R.J.; Cox, G.N Mol. Blochem. Parasitol. 37, 73-86, 1989
A;Title: Cuticle collagen genes of Haemonchus contortus A;Reference number: A44984; MUID:90136718; PMID:2615789
A;Accession: B44984
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                                                                                                              A;Molecule type: mRNA
A;Residues: 1-210 <SHA>
A;Cross-references: GB:J04671; GB:J04670
                                                                                                  C; Superfamily: unassigned
                                                                                                                                                                                                                                  C; Accession:
                                                                                                                                                                                                                                              C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change
                                                                                                                                                                                                                                                          C; Species: Haemonchus contortus
                                                                                                                                                                                                                                                                      collagen -
                                                                                                                                                                                                                                                                                    B44984
                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 11; Conser
                                                 Matches
                                                               Query Match
Best Local
                                                             Local
                                                                                                                                                                                                                                                                                                                                        1328
151
                                                                                                                                                                                                                                                                      nematode (Haemonchus contortus) (fragment)
                      57
                                                                                                                                                                                                                                                                                                                                                                 71
                                                 10;
                                                            Similarity
                                                                                                                                                                                                                                  B44984
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                      GAPGAPGEKG
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                                                Conservative
                      66
                                                            4.1%;
160
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                                                            Score; Pred.
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                                                   Mismatches
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                                                                           210;
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                                                Gaps
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A;Cross-references: GB:J03542; NID:g165705; PIDN:AAA31465.1; PID:g165706
A;Note: 12-Pro was also found
A;Note: two species of mRNA, which appear to be transcribed from a single gene,
A;Note: the amino end of the mature protein is blocked
C;Comment: Pulmonary surfactant is a complex of phospholipids and proteins that
C;Comment: This protein is a sialoglycoprotein synthesized by alveolar type II c
pendent on the presence of calcium ions
C;Superfamily: mannose-binding lectin; C-type lectin homology
C;Superfamily: mannose-binding lectin; C-type lectin bomology
C;Keywords: acetylated amino end; alveolar proteinosis; calcium; gaseous exchang
F;1-15/Domain: signal sequence #status predicted <SIG>
F;1-6-247/Product: pulmonary surfactant protein A #status predicted <MAT> N;Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactan C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999 R;Boggaram, V.; Qing, K.; Mendelson, C.R. J. Biol. Chem. 263, 2939-2947, 1988 A;Title: The major apoprotein of rabbit pulmonary surfactant. A;Reference number: A29931; MUID:88139348; PMID:2830270 C; Accession: A29931 pulmonary surfactant protein A precursor - rabbit LNRBPS A; Molecule type: mRNA A; Residues: 1-247 < BOG> A;Accession: A29931 27-99/Region: collagen-like pulmonary surfactant-associat Elucidation of primary cells. could

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C;Superfamily: mannose-binding lectin; C-type lectin homology C;Keywords: acetylated amino end; alveolar proteinosis; calcium; gaseous F;1-20/Domain: signal sequence #status predicted <SIG> F;21-248/Product: pulmonary surfactant protein A #status predicted <MAT> F;127-246/Domain: C-type lectin homology <LCH> F;127-246/Domain: C-type lectin homology <LCH> F;21/Modified site: acetylated amino end (Glu) (in mature form) #status F;30,33,66,42,54,57,63,76,79,82,91,97/Modified site: 4-hydroxyproline (P. F;207/Binding site: garbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pulmonary surfactant protein A precursor (clone 1A) - human
N;Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associated
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C;Accession: B25720
R;Floros, J.; Steinbrink, R.; Jacobs, K.; Phelps, D.; Kriz, R.; Recny, M.; Sultzman, L.;
J. Biol. Chem. 261, 9029-9033, 1986
A;Title: Isolation and characterization of cDNA clones for the 35-kDa pulmonary surfacta
A;Accession: B25720
A;Molecule type: mRNA
A;Residues: 1-248 cFLO>
A;Cross-references: GB:K03475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:K03475
A;Note: part of the sequence was confirmed by protein sequencing
A;Note: the amino end of the mature protein, which was not identified,
A;Note: clones corresponding to two different proteins were sequenced.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 10q22-10q23
                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: GDB:SFTPA1; SFTP1; SP-A; SP-A1
A;Cross-references: GDB:119593; OMIM:178630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: mannose-binding lectin; C-type lectin homology
(;Keywords: acetylated amino end; alveolar proteinosis; calcium; gaseous exchange;
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-248/Product: pulmonary surfactant protein A #status predicted <MAT>
F;127-246/Domain: C-type lectin homology <LCH>
F;127-246/Domain: C-type lectin homology <LCH>
F;21/Modified site: acetylated amino end (Glu) (in mature form) #status predicted
F;30,33,36,42,54,57,63,76,79,82,91,97/Modified site: 4-hydroxyproline (Pro) #status
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A;Note: part of the sequence was confirmed by protein sequencing
A;Note: the amino end of the mature protein, which was not identified, is partially acet
A;Note: clones corresponding to two different proteins were sequenced. Cotranslational #
C;Genetics:
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A;Accession: A25720
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A;Title: Isolation and characterization of cDNA clones for the 35-kDa pulmonary surfactant A:Reference number: A25720; MUID:86250832; PMID:3755136
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C; Superfamily: n
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A;Cross-references: GDB:119593; C
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A;Cross-references: GB:
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N;Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associated
                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                              Score 10;
Pred. No.
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Pred. No.
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                              DB 1;
0.13;
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. 0.13;
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                                                                             pulmonary surfactant protein A precursor - rat
N;Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associ
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text_change 16-Jul-1999
C;Accession: A29299; JS0034; S23183
R;Sano, K.; Fisher, J.; Mason, R.J.; Kuroki, Y.; Schilling, J.; Benson, B.; Voelker
R;Sano, K.; Fisher, J.; Mason, R.J.; Kuroki, Y.; Schilling, J.; Benson, B.; Voelker Biochem. Biophys. Res. Commun. 144, 367-374, 1987
A;Title: Isolation and sequence of a cDNA clone for the rat pulmonary surfactant-as A;Reference number: A29299; MUID:87213191; PMID:3579914
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F;28-102/Region: collagen-like
F;127-246/Domain: C-type lectin homology <LCH>
F;20,207/Binding site: carbohydrate (Asn) (cover)
F;30/Modified site: 4-hydroxyproline (Pro) #sta
                                                                                                                                                                                                                                                                                  pendent on the presence of calcium ions.
(Superfamily: mannose-binding lectin; C-type lectin homology
(Keywords: alveolar proteinosis; calcium; disulfide bond; gaseous exchange;
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-248/Product: pulmonary surfactant protein A #status experimental <MPT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Roscidues: 18-32 <LIA>
A;Residues: 18-32 <LIA>
R;Ross, G.F.; Meuth, J.; Ohning, B.; Kim, Y.; Whitsett, J.A.
Blochim. Biophys. Acta 870, 267-278, 1986
A;Title: Purification of canine surfactant-associated glycoproteins A.
A;Reference number: A60142; MUID:86159848; PMID:3006781
A;Accession: A60142
                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: A93388; MUID:87115834; PMID:3808053
A;Contents: annotation; animal lectin domain homology
C;Comment: Pulmonary surfactant is a complex of phospholipids and proteins that low
C;Comment: This protein is a sialoglycoprotein synthesized by alveolar type II cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: part of the sequence, including the amino end on R;Liau, D.F.; Ryan, S.F. Chem. Phys. Lipids 59, 29-38, 1991
A;Title: Purification of surfactant protein A from dog A;Reference number: A61227; MUID:92163993; PMID:1790579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associ C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1987 #sequence revision 30-Sep-1987 #text_change 16-Jul-1999
C;Accession: A25296; A61227; Ā60142
R;Benson, B.; Hawgood, S.; Schilling, J.; Clements, J.; Damm, D.; Cordell, B.; Whit Proc. Natl. Acad. Sci. U.S.A. 82, 6379-6383, 1985
A;Title: Structure of canine pulmonary surfactant apoprotein: cDNA and complete ami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 325, 490, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Patthy,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-248 <BEN>
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                                               45 GLPGRDGRDG 54
                                                                                                    l Similarity
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Pred. No. 0.13;
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                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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                                                                                         Gaps
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C;Comment: Pulmonary surfactant is a complex of phospholipids and proteins that lowers C;Comment: This protein is a sialoglycoprotein synthesized by alveolar type II cells. I pendent on the presence of calcium ions.

C;Comment: Two species of mRNA, which probably are transcribed from a single gene, have C;Comment: Size heterogeneity of these proteins arises from posttranslational modificat C;Superfamily: mannose-binding lectin; C-type lectin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: I51921
R;Katyl, S.L.; Singh, G.; Locker, J.
R;Katyl, S.L.; Singh, G.; Locker, J.
Am. J. Respir. Cell Mol. Biol. 6, 446-452, 1992
A;Title: Characterization of a second human pulmonary surfactant-associated protein SP-A;Reference number: I51921; MUID:92198680; PMID:1372511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Rat pulmonary surfactant protein A is expressed as two A;Reference number: JS0034; MUID:89000785; PMID:2901856 A;Contents: 1.6 kb cDNA A;Accessibn: JS0034 A;Accessibn: JS0034 A;Molecule type: mRNA A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      묽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-32 < LAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eur. J. Biochem. 206, 613-623, 1992
A;Title: Characterization of the rat pulmonary surfactant protein A promoter.
A;Reference number: S23183; MUID:92298987; PMID:1608951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Contents: 0.9 kb cDNA
A; Accession: A29299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: SP-Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-248 <FI6>
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A;Residues: 1-248 <SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pulmonary surfactant-associated protein A1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S23183
                                                                                                                                                                                               A; Map position: 10q22-10q23
                                                                                                                                                                                                                            A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;127-246/Domain: C-type lectin homology <LCH>;21/Binding site: carbohydrate (Asn) (covalent) #status absent;31/Binding site: carbohydrate (Asn) (covalent) #status absent;30,33,36,42,54,57,63,67,70,76/Modified site: 4-hydroxyproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Keywords: alveolar proteinosis; calcium; gaseous exchange; glycoprotein; hydroxyproli;1-20/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                    Gene: GDB:SFTPA1;
                                                                                                                                                                                                                                                                                                                                                                                                                          Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-248/Product: pulmonary surfactant 37-109/Region: collagen-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: the codons given Lacaze-Masmonteil, T.;
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                                                                                                                                                                                                                                                                                                        Cross-references: GB:M68519; NID:g338048; PIDN:AAA60319.1; PID:g338049
                                                                                                                                                                                                                                                                                                                                           Molecule type: DNA
Residues: 1-248 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary; translated from GB/EMBL/DDBJ
           Local
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Biophys. Acta 950, 338-345, 1988
                                                                                                                                                                     58/1; 98/1; 1
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                                                                                                                                     mannose-binding lectin; C-type lectin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                              C-type lectin homology <LCH>
                                                                                                                                                                                                                            GDB:119593; OMIM:178630
                                                                                                                                                                                                                                                       SFTP1; SP-A; SP-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence #status predicted <SIG>
nonary surfactant protein A #status experimental <MAT>
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100.0%; *.
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100.0%; Pred. No. 0.:
ive 0; Mismatches
  Score 10; DB 2; pred. No. 0.13; 0; Mismatches
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                                                          Length 248;
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Search completed: June 20, 2003, 11:43:37 Job time: 22 secs

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A;Cross-references: GB:S48768; NID:g260452; PIDN:AAB24274.1; PID:g260453 A;Note: sequence extracted from NCBI backbone (NCBIN:118740, NCBIP:118741) C;Superfamily: mannose-binding lectin; C-type lectin homology F;127-246/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                    A;Title: Murine pulmonary surfactant SP-A gene: cloning, A;Reference number: A48853; MUID:93072386; PMID:1443158 A;Contents: DBA/2J
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                                                                                                                                                                                                                                                                                 A; Accession: A48853
                                                                                                                                                                                                                                                                                                                                                                                                             pulmonary surfactant-associated protein SP-A - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Aug-1999
                                                                                                                                                                                                                          A;Residues: 1-248 <KOR>
                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: A48853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
                                                                                                                                                                                                                                         A; Molecule type: nucleic acid
                                                                          Matches
                                                                                            Query Match
Best Local
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                                                                                          Local
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                             45 GLPGRDGRDG 54
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                                                                                      100.0%;
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                                                                                        Score 10;
Pred. No.
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                                                                                        DB 2;
0.13;
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                                                                                                                                                                                                                                                                                                                                      sequence,
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Result
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
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Match
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                     CQTS HUMAN
CQT7 HUMAN
PSPD BOVIN
PSPD BOVIN
PSPD RAT
PSPD RAT
PSPD HUMAN
CA21 RANCA
CA34 HUMAN
CAC2 HAECO
PSPA CANFA
PSPA CANFA
PSPA CANFA
PSPA RABIT
CAF1 EPHMU
CA13 BOVIN
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P02465 bos taurus
O46392 canis famil
P41110 oryctolagus
P02463 mus musculu
P31722 rattus norv
P49913 homo sapien
P23435 homo sapien
                                                                                                                                                                               P49874 sus scrofa
Q28668 oryctolagus
P18856 ephydatia m
P04258 bos taurus
P08121 mus musculu
P02461 homo sapien
P57012 neisseria m
P13941 rattus norv
Q06335 mus musculu
P15943 rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P35247 homo sapien
O42350 rana catesb
Q01955 homo sapien
Q02388 homo sapien
P16252 haemonchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9bxj0 homo sapien
Q9bxj2 homo sapien
P35246 bos taurus
P50404 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                 P07714 homo sapien
P35242 mus musculu
P08427 rattus norv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P50403 cavia porce
P12842 oryctolagus
P06908 canis famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P35248 rattus norv
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CQT5_HUMAN STANDA

AC Q9BXJ0; Q9UFX4;

DT 15_HUN-2002 (Rel. 41.
  Best Local Similarity 100.0%; Pred. No. 1.9e-193; Matches 243; Conservative 0; Mismatches 0;
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VP36_MOUSE	VP36 CANFA	CQT4_HUMAN	CC13 CAEEL	CC12_CAEEL	CC40_CABEL	CC02_CAESL	APM1 MOUSE	APM1_HUMAN	CERL_RAT	CERL_HUMAN	CERB MOUSE
Q9dbh5	P49256	Q9bxj3	£20631	_	-	P17656	Q60994	Q15848	P98087	Q9ntu7	Q9r171
mus musculu	canis famil	homo sapien	caenorhabdi	caenorhabdi	caenorhabdi	caenorhabdi	mus musculu	homo sapien	rattus norv	homo sapien	mus musculu

ALIGNMENTS

PRT;

243 A

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EMBL; AF3 EMBL; AL1 Genew; HG InterPro; InterPro; InterPro; Pfam; PF0 Pfam; PF0 Pfam; PF0 Pfam; PF0 Collagen; SIGNAL CHAIN DOMAIN		
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NEG. POTENTIAL. CONFLEMENT-CIQ TUMOR NECROSIS RELATED PROTEIN 5. COLLAGEN-LIKE. C1Q.	A.A. ar B., Mewes HW., Gassenhuber the EMBL/GenBank/DDBJ databases I COLLAGENOUS DOMAIN. 1 COL DOMAIN. 1 CIQ DOMAIN. 1 CIQ DOMAIN. 1 CIQ FIRE A COMPAIN. 1 CIQ FIRE A COMPAIN. 1 CIQ FIRE A COMPAIN. 1 CIQ DOMAIN. 1 COPYTIGHT. It is produced through a mod the compart of the comparation and the comparation as long as its contentiutions as long as its content that is not removed. Usage by use agreement (See http://www.ise@isb-sib.ch).	Created) Last sequence update) Last sequence update) Last annotation update) necrosis factor-related protein 5 pre necrosis factor-related protein 5 pre Chordata; Craniata; Vertebrata; Butele Primates; Catarrhini; Hominidae; Homo. J.M.; J.M.; J.M.; J.M.; The EMBL/GenBank/DDBJ databases.
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15-JUN-2002
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
-!- SIMILARITY: CONTAINS 1 CIQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complement-clq tumor necrosis factor-related ClQTNP7 OR CTRP7.
                   DOMAIN
DOMAIN
                                                                                   SIGNAL
                                                                                                                                                                                                                                EMBL; AF329839; AAK17963.1; -.
EMBL; BC022187; AAH22187.1; -.
Genew; HGNC:14342; C1QTNF7.
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InterPro; IPR000087; Collagen.
Pfam; PP00386; Clq; 1
Pfam; PP01391; Collagen; 2.
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Mammalia; Eutheria;
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Q9BXJ2;
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Homo sapiens compl
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                                                                                                                         PR00007; Cum.
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 289 AA;
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141
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                                                                                                                                                  COMPLEMNTC1Q.
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276
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lement-clq tumor necrosis factor-related protein.";
)) to the EMBL/GenBank/DDBJ databases.
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Primates;
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COMPLEMENT-C1Q TUMOR
RELATED PROTEIN 7.
COLLAGEN-LIKE.
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Catarrhini; Hominidae,
 A61609FF86D26946 CRC64;
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Matches
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RESULT 3

PSPD_BOVIN
ID PSPD_BOVIN
ID PSPD_BOVIN
AC P35246;
AC P35
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L Immunology 78:159-165 (1993).

C -i- FUNCTION: CONTRIBUTES TO THE LUNG'S DEFENSE AGAINST INHALED

C MICROORGANISMS. BINDS STRONGLY MALTOSE RESIDUES AND TO A LESSER

C EXTENT OTHER ALPHA-CLUCSYL MOIETIES. IT COULD BARTICIPATE IN THE

EXTERACELLULAR REORGANIZATION OR TURNOVER OF PULMONARY SURFACTANT.

C -i- SUBGUNIT: OLIGOMERIC COMPLEX OF 4 SET OF HOMOTRIMERS.

C -i- SUBCELLULAR LOCATION: EXTRECTANT CONSISTS OF 90% LIPID AND 10%

C -I- MISCELLANEOUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND 10%

PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS,

C CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL

C -I- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                           Pfam; PF00059; lectin_c; 1.
Pfam; PF01391; Collagen; 2.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extrement by the European Bioinformatics Institute. There are no restruct use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lim B.L., Lu J., Reid K.B.M.;
"Structural similarity between bovine conglutinin and bovine "Structural similarity between bovine of liver as a site of
                                                                                                                                                                                                PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Calcium; Surface film; Gaseous
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Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Cet
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Pulmonary surfactant-associated protein D precursor (SP-D)
                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000087; Collagen.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S33603; S33603.
HSSP; P35247; 1B08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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11; Conservative 0;
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                                                                                                                                                  Repeat; Coiled coil
BY SIMILARITY.
COILED COIL (POTENTIAL).
C-TYPE LECTIN (SHORT FORM)
BY SIMILARITY.
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COLLAGEN-LIKE
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Best Local
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2001) to THE LUNG'S DEFENSE AGAINST
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STRAIN=C57BL/6 X CBA; TISSUE=Lung;
MEDLINE=96094460; PubMed=7499852;
Motwani M., White R.A., Guo N., Do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P50404;
01-OCT-1996
01-OCT-1996
                                          This
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STRAIN=129/Sv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (OCT-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99244602; PubMed=10226065; Lawson P.R., Perkins V.C., Holmsko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Mouse surfactant protein-D. cDNA cloning, localization to chromosome 14.";
J. Immunol. 155:5671-5677(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia;
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01-OCT-1996 (Rel.
15-JUN-2002 (Rel.
                                                                     FUNCTION: CONTRIBUTES TO THE LUNG'S DEFENSE AGAINST INHALED MICROORGANISMS. BINDS STRONGLY MALTOSE RESIDUES AND TO A LESSER EXTENT OTHER ALPHA-GLUCOSYL MOIETIES. IT COULD PARTICIPATE IN THE EXTRACELLULAR REORGANIZATION OR TURNOVER OF PULMONARY SURFACTANT. SUBCELLULAR LOCATION: EXCTRACEIVLLAR COMPLEX OF 4 SET OF HOMOTRIMERS.

SUBCELLULAR LOCATION: EXCTRACIANT CONSISTS OF 90% LIPID AND 10% PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS, PULMONARY SURPACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS, CARBOHYDRATE-BINDING GLYCOPOTEINS (SP-A AND SP-D) AND 2 SMALL HYDROPHOBIC PROTEINS (SP-B AND SP-C).

SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Respir.
SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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protein-D regulates surfactant phospholipid homeostasis
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Sciurognathi;
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DISULFID
CARBOHYD
SEQUENCE
collagenous surfactant-associated protein.";
Biochemistry 28:6361-6367(1989).
                                     Persson A., Chang D., Rust K., Moxley M., Longmore "Purification and biochemical characterization of o
                                                                      TISSUE=Lung;
MEDLINE=90001186; PubMed=2675969;
                                                                                                             SEQUENCE OF 73-95 AND 153-180
                                                                                                                                              "Primary structure of rat pulmonar deduced amino acid sequence.";
J. Biol. Chem. 267:1853-1857(1992)
                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
                                                                                                                                                                                                                          Shimizu H.,
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.,
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PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Calcium; Surface film; Gaseous
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EMBL; AF047741; AAD31380.1;
EMBL; AF192134; AAF15277.1;
EMBL; BC003705; AAH03705.1;
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InterPro; IPR000087; Collagen.
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28, Last sequence up
38, Last annotation
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                                                                                                                                                                                                                                                                                                                                    ; Chordata;
; Rodentia;
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Sciurognathi;
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protein D precursor (SP-D)
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                                                                                                                                                                                                                                                                                                                                                  Vertebrata;
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0.074;
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CP4 (SP-D),
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DISULFID
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DOMAIN
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PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Calcium; Surface film; Gaseous exchange; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                   Pulmonary surfactant-associated SFTPD OR SFTP4 OR PSPD.
                                                                                                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal; Lectin; SIGNAL
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InterPro; IPR001304; Lectin_C.
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                                                                                                       NAMUH_DASA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: OLIGOMERIC COMPLEX OF 4 SET OF HOMOTRIMERS.
SUBCELLAURA LOCATION: EXCURACIANT OP 90% LIPID AND 10%
MISCELLABEDUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND 10%
PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS,
CARROHYDRATE BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL
HYDROPHOBIC PROTEINS (SP-B AND SP-C).
$IMILARITY: CONTAINS A COLLAGENOUS DOMAIN.
$IMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: CONTRIBUTES TO THE LUNG'S DEFENSE AGAINST INHALED MICROORGANISMS. BINDS STRONGLY MALTOSE RESIDUES AND TO A LESSER EXTENT OTHER ALPHA-GLUCOSYL MOIETLES. IT COULD PARTICIPATE IN THE EXTRACELLULAR REORGANIZATION OR TURNOVER OF PULMONARY SURFACTANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
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  Craniata; Ve
Catarrhini;
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 Vertebrata; Euteleostomi; i; Hominidae; Homo.
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  Glycoprotein; Calcium; Surface Film; Gaseous exchange; Hydroxylation; Signal; Lectin; Collagen; Repeat; Coiled coil; 3D-structure.
                                            Pfam; PF00059; lectin_c; 1.
Pfam; PF01391; Collagen; 4.
SMART; SM00034; CLECT; 1.
                                                                                                 Genew; HGNC:10803; SFTPD.
MIM; 178635; -.
                                                                                                                         PIR; A45225; A45225.
PIR; S18382; S18382.
PDB; 1808; 29-NOV-99
                                                                                                                                                         EMBL; L05485; AAB59450.1;
EMBL; L05483; AAB59450.1;
EMBL; L05484; AAB59450.1;
EMBL; X65018; CAA46152.1;
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Biochem. J. 284:795-802
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entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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Structure 7:255-264(1999).
-!- FUNCTION: CONTRIBUTES TO THE LU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crouch E., Rust K., Veile R., Donis-Keller H., Grosso L., "Genomic organization of human surfactant protein D (SP-D). SP-D encoded on chromosome 10922.2-23.1.";
J. Biol. Chem. 268:2976-2983(1993).
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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PTM: The N-terminus is blocked.

MISCELLANGOUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND 10%

MISCELLANGOUS: PULMONARY SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS.

CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL

HYDROPHOBIC PROTEINS (SP-B AND SP-C).

SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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between
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type I collagen of bullfrog Rana catesbeiana.
Gene 194:283-289(1997).
-I- FUNCTION: TYPE I COLLAGEN IS A MEMBER OF
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Amphibia; Batrachia
NCBI_TaxID=8400;
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Eukaryota; Metazoa; Chordata;
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                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See l
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PTM: PROLINES A'
UNIT (G-X-Y) AR
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SUBUNIT: TRIMERS OF ONE ALPHA 2(I) AND TWO ALPHA 1(I) CHAINS TISSUE SPECIFICITY: FORMS THE FIBRILS OF TENDON, LIGAMENTS A
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IPR000885;
                                                                                            email to license@isb-sib.ch).
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Pfam; PF01410; COLFI; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mariyama M., Leinonen A., Mochizuki T., Tryggvason K., Reeders "Complete primary structure of the human alpha 3(IV) collagen coexpression of the alpha 3(IV) and alpha 4(IV) collagen chains
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94364994;
Mariyama M., Leinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                    Quinones S., Bernal D., Garcia-Sogo M., Elena S.F., Saus J.; "Exon/intron structure of the human alpha 3(IV) gene encompassing Goodpasture antigen (alpha 3(IV)NC1). Identification of a potential antigenic region at the triple helix/NC1 domain junction."; J. Biol. Chem. 267:19780-19784 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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SEQUENCE OF 1453-1670 FROM N.A.
MEDLINE=91353570; PubMed=1882840;
Morrison K.E., Mariyama M., Yang-
                                                                                                                                                                                                    SEQUENCE OF 1386-1670 FROM N.A., MEDLINE=93015826; PubMed=1400291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leinonen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human
                                                                                                                                                                                                                                                                                               autosomal Alport syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol.
                                                                                                                                                                                                                                                                       Am.
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                                                                                                                                                                                                                                                                       Soc. Nephrol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (OCT-1998)
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1355
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82
1093
1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=8083201;
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1256
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the EMBL/GenBank/DDBJ databases
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COLLAGEN ALPHA 2 (1
CARBOXYL-TERMINAL
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N-LINKED (GLCNAC. . .)
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Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CB793AD5D6F41D2A CRC64;
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                                                                                                                                                                                                                             AND PARTIAL
                                                                                                                                                                                                                                                                                                                                         Cohen-Solal L.,
Antignac C.;
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VARIANTS R-43;
                                                                                                                                                                                                                                                                                                                        mutations
                                                                                                                                     potentially
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Yang-Feng

T.L.,

Reeders

S.T.;

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recessive Alport syndrome.";
Hum. Mol. Genet. 3:1269-1273 (1994).
-i- FUNCTION: TYPE IV COLLAGEN IS THE
GLOMERCULAR BASEMENT MEMBRANES (GI
MESHWORK TOGETHER WITH LAMININS,
                                                                                                                                                                                                                                                                                                                    Barrientos A.,
                                                                                                                                                                                                                                                                                                                               MEDLINE=95078827; PubMed=7987301;
Lemmink H.H., Mochizuki T., van d
                                                                                                                                                                                                                                                                                                                                                                                                                    Bernal D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  collagen gene. Differential expression of the human alpha 3(IV) predict three protein variants with distinct carboxyl regions.", [9]
                                                                                                                                                                                                                                                                                      Parrientos A., Monnens L.A.H., van Oost B.A., Brunn Reeders S.T., Smeets H.J.M.;
Mutations in the type IV collagen alpha 3 (COL4A3)
                                                                                                                                                                                                                                                                                                       Reeders S.T.,
                                                                                                                                                                                                                                                                                                                              Lemmink H.H., Mochizuki
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93280184; PubMed=8505332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence and localization of a partial cDNA encoding the 3 chain of type IV collagen.", Am. J. Hum. Genet. 49:545-554(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-29, FROM N.A. MEDLINE=98196854; PubMed=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Alternative splicing of the NC1 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1439-1670,
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to be the alpha 3 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94124597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Kidney;
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                                     COCHLEA, LUNG AND BRAIN.

DOMAIN: ALPHA CHAINS OF TYPE IV CO

DOMAIN (NC1)'AT THEIR C-TERMINUS,

G-X-Y REPEATS IN THE LONG CENTRAL

CAUSE FLEXIBILITY IN THE TRIPLE HE

TRIPLE-HELICAL 7S DOMAIN.
                                                                                                       WITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN SUBCELLULAR LOCATION: CELL SURFACE (POTENTIAL). ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; 1 (SHE 3/L5; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY C-TERMINAL NC1 DOWAINS.

TISSUE SPECIFICITY: ALPHA 3 AND ALPHA 4 TYPE IV (COLCCALIZED AND PRESENT ONLY IN BASEMENT MEMBRANE)
                                                                                                                                                                 NIDOGEN.
SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS,
ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELI
WITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN
WITH 2 OTHER CHAINS TO GENERATE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clin. Invest.
                                                                                                                                                                                                                                                                                                                                                                                                  human mRNA encoding the Goodpasture antigen is alternatively
PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. THE ALTERNATIVE SPLICED FORM V CONTAINS AN ADDITIONAL
                                                                                                                                                                                                                                                                                                                                                                                 Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugimoto M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COL4A3 and
                                                                                                                                                                                                                                                                                                                                                                             268:12090-12094(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ng of the human Goodpasture antigen demonstrates 3 chain of type IV collagen."; 89:592-601(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=9537506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=8294492;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COL4A4 coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND ALTERNATIVE SPLICING
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                                                                                                                                                                                                                                          THE MAJOR STRUCTURAL COMPONENT (GBM), FORMING A 'CHICKEN-WIRE'
                                                            COLLAGEN HAVE A NONCOLLAGENOUS S, FREQUENT INTERRUPTIONS OF THE AL TRIPLE-HELICAL DOMAIN (WHICH )
                                                                                                         ALPHA 4 TYPE IV COLLAGENS ARE BASEMENT MEMBRANES OF KIDNEY,
                                                HBLIX),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kigasawa
                                                                                                                                                                                                                                 PROTEOGLYCANS
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                                                  AND
                                                                                                                                                                               ISOFORMS, ALPHA 1(IV)
RIPLE HELIX STRUCTURE
COLLAGEN NETWORK.
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                                                                                                                                                                                                                                                                                                                  Brunner
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                                                                                                                                              (SHOWN HERE), THEY DIFFER IN
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                                                SHORT N-TERMINAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome
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PTM: TYPE IV COLLAGENS ARE INVOLVED IN INTER-
IV COLLAGENS.
                                                  N-LINKED GLYCOSYLATION
             LOCATED
          NTER- AND INTRAMO
                                 SITE.
CONTAIN NUMEROUS
                     INTRAMOLECULAR DISULFIDE
          ARE CONSERVED
            Z
         RESIDUES WHICH
IDE BONDING. 12 OF
IN ALL KNOWN TYPE
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PYM: Phosphorylated by the Goodpasture antigen-binding protein.
DISEASE: ANTIGODIES AGAINST THE NCI DOMAIN OF ALPHA3(IV) MEDIATE
THE HUMAN AUTOINMUNE DISEASE, GOODPASTURE SYNDROME, WHICH IS
CHARACTERIZED BY HEMATURIA AND PULMONARY HEMORRHAGE.
DISEASE: DEFECTS IN COL4A3 ARE ASSOCIATED WITH THE TYPE I
AUTOSOMAL RECESSIVE FORM OF ALFORT SYNDROME, AN HEREDITARY
GLOMERULONEPHROPATHY CHARACTERIZED BY PROGRESSIVE RENAL FAILURE,
HEMATURIA AND DEAFNESS. THE RECESSIVE FORM OCCURS EQUALLY BETWEEN AND FEMALES

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or send an between AJ288527; AJ288528; AJ288529; AJ288530; AJ288531; AJ288532; AJ288533; AJ288533; AJ288518; AJ288519; AJ288520; AJ288487; AJ288488; AJ288489; AJ288490; AJ288491; AJ288491; AJ288492; AJ288493; AJ288510; AJ288511; AJ288494; AJ288495; AJ288524; AJ288517; AJ288508; CAA56335 CAC36101 CAC3610 CAC361 CAC36101 JOINED
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Matches
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CA17 HUMAN STANDARD;
Q023B8; Q14054; Q16507;
Q1_JUN-1994 (Rel. 29, Cr
Q1_FEB-1996 (Rel. 33, La
15_JUN-2002 (Rel. 41, La
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Christiano A.M., Greenspan D.S., Lee S., Uitto J.;
"Cloning of human type VII collagen. Complete primary
alpha 1(VII) chain and identification of intragenic po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                       MEDLINE=93338437; PubMed=1307247
Christiano A.M., Rosenbaum L.M.,
Woodley D.T., Pan T.C., Zhang R.
                                                                                              Gammon W.R., Abernethy M.L., Padilla K.M., Prisayanh P.S., Cook M.E., Wright J., Briggaman R.A., Hunt S.W. III; "Noncollagenous (NCI) domain of collagen VII resembles multidomain
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.
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          MEDLINE=92231902; PubMed=1567409;
Tanaka T., Takahashi K., Furukawa
                                                                          adhesion proteins involved extracellular matrix.";
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                                                                                                                                             SEQUENCE OF
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Bauer E.A., Ma
                                                                                                                                                                                                                        SEQUENCE OF 815-1439 FROM N.A.
MEDLINE=91334380; PubMed=1871109;
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"Molecular cloning
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AJ288537; CAC36101.1,
AJ288538; CAC36101.1,
M92993; AAA21610.1;
M92993; AAA21610.1;
M81379; AAA51556.1;
M81379; AAA51544.1;
U02519; AAA18942.1;
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93338437; PubMed=1307247;
93338437; PubMed=1307247;
M. Rosenbaum L.M., Chung-Honet L.C., Parente
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                                                                 Dermatol.
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                                                                                                                                                                                      ., Chung L.C., Ryynaenen J., Woodley D.T., Mattei M.-G., Chu M.-L., Uitto J.; VII collagen: cDNA cloning and chromosoma
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Christiano A.M., Lee J.Y.-Y., Chen W.J., I Pretibial epidermolysis bullosa: genetic identification of a glycine-to-cysteine su helical domain of type VII collagen."; Hum. Mol. Genet. 4:1579-1583(1995).
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Gly-->Ser substitution in the triple-helical
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Christiano A.M., Greenspan D.S., Hoffman G
Lin A.N., Dietz H.C., Hovnanian A., Uitto
"A missense mutation in type VII collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98041696;
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genotype/phenotype
severity.";
                                                                                                                                                                             MEDLINE=96220218; PubMed=8644729;
Christiano A.M., McGrath J.A., Tan K.C., Uitto J.;
"Glycine substitutions in the triple-helical region of type
collagen result in a spectrum of dystrophic epidermolysis
                                                                                                                                                                                                                                                                                                                                                                                       Cavalieri R., Uitto J.;
                                                                                                                                                                                                                                                                                                                                                                                                              Christiano A.M., Morricone A.,
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Am. J. Hum.
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type VII collagen in a
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agenous NC-2 domain and intron,
esponding region of the COLTA1
Mol. Genet. 2:273-278(1993).
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Genet. 58:671-681(1996).
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Hoffman G.G., Chung-Honet
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PubMed=8499916;
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"Clinicopathological correlations of compound humutations in recessive dystrophic epidermolysis J. Invest. Dermatol. 107:171-177(1996).
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MEDLINE=96183562; Pub
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Naylor S.L., Kerbacher K., Zimmermann M., Krajci
Gedde-Dahl T. Jr., Bruckner Tuderman L.;
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Terracina M., Posteraro P., Schubert M.,
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Luger T., Bruckner-Tuderman L.;
                                                                                                                                                                                                                                                                                                                               MEDLINE=98334662; PubMed=9668111;
                                                                                                                                                                                                                                                                                                                                                                          Hum.
                                                                                                                                                                                                                                                                                                                                               VARIANTS DDEB
 VARIANTS
                                                                                                                                                                                                        MEDLINE=98410969;
                                                                                                                                                                                                                       VARIANTS DEB CYS-2008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Hum. Genet. 61:599-610(1997)
                                                                                                                                                                                                                                                                                                                                                                                       gene.";
                                                                                                                                                                                           Pulkkinen L.,
DEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7465605; PubMed=9326325;
A., Rochat A., Bodemer C., P., Christiano A.M., Uitto J.,
                                                                                                                                                                                                                                                                                                                                                                          Genet. 6:1125-1135(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dermatol.
                                                                                                                                                 Dermatol.
TRP-2034;
                                                                                                                                                                                                                                                                                                                                               ASP-1519;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=8757758;
                                                                                                                                                                                                       PubMed=9740253
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                                                                                                                                                   111:534-537(1998).
                                                                                                                                                                           Ishida-Yamamoto
ns in dystrophic
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VAL-2040;
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 ARG-2043;
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VII, loss of
                                                                                            Sonego G.,
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  ARG-2064
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M., Bar
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ci P.,
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01-OCT-1996
01-OCT-1996
16-OCT-2001
Pulmonary su
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15-JUN-2002
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01-AUG-1990
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Haemonchus contortus (Barber pole worm).
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99072663; PubMed=9856843;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shamansky L.M., Pratt D., Boisvenue R.J., "Cuticle collagen genes of Haemonchus con
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J04670; AAA29172.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90136718; PubMed=2615789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01391; Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Parasitol. 37:73-86(1989).

FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGE PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT.

MISCELLANEOUS: THIS PROTEIN SHOWS 4 POTENTIAL TRIPLE-HELICA REGIONS, WHICH CONTAIN GLYCINE AS EVERY THIRD AMINO ACID.

MISCELLANEOUS: IN ALL NEMATODE CUTICLE COLLAGENS, THE POLYF CHAINS ARE COMPLEXED WITHIN THE CUTICLE BY DISULFIDE BONDS: OTHER TYPES OF COVALENT CROSS-LINKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE CUTICULAR COLLAGEN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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96 (Rel. 34, Created)
96 (Rel. 34, Last sequence update)
11 (Rel. 40, Last annotation updat
surfactant-associated protein A p
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                                                                                                                                                                                                                                                                                                                                              tissue; Repeat; Multigene family; Collagen
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Pred. No.
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0.38;
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0.31;
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protein A pre

precursor

(SP-A)

(PSP-A)

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RESULT 12
PSPA RABIT
ID PSPA
AC P1284
AC P1286
DT 01-OC
DT 01-OC
DT 16-OC
                                                                                                                                                                                                        В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning of guinea pig surfactant protein A defines a distinct cellular distribution pattern within the lung.";

LAM. J. Physiol. 273:L900-L906(1997).

C. -!- FUNCTION: IN PRESENCE OF CALCIUM IONS, PSAP BINDS TO SURFACTANT COMPRESENCE OF CALCIUM IONS, PSAP BINDS TO SURFACTANT COMPLETIAL FOR NORMAL RESPIRATION.

C. AIR-LIQUID INTERFACE IN THE ALVEOLI OF THE MAMMALIAN LUNG AND IS CESENTIAL FOR NORMAL RESPIRATION.

C. -!- SUBGUNIT: OLIGOMERIC COMPLEX OF 6 SET OF HOMOTRIMERS.

-!- MISCELLANEOUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND 10% PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS, HYDROPHOBEL PROTEINS (SP-A AND SP-C) AND 2 SMALL -!- SIMILARITY: CONTAINS A COLLAGENOUS.
                                                                                                                                                          Matches
                                                                                                                                                                      Query Match
Best Local :
   RABIT
PSPA RABIT
P12842;
01-OCT-1989
01-OCT-1989
16-OCT-2001
                                                                                                                                                                                                                             DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                        CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                               Signal;
                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                   PROSITE;
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InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
Pfam; PF01391; Collagen; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                       Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U40869; AAB82952.1; -. HSSP; P22897; 1EGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Hartley; TISSUE=Lung; MEDLINE=98018900; PubMed=9357868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cavia porcellus (Gui
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10141;
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SFTPA1 OR SFTPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content liftled and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYDROPHOBIC PROTBINS (SP-B AND SP-C).
SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                            45 GLPGRDGRDG
                                                                                                             39
                                                                                                                                                          10;
                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                          Lectin;
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PS50041; C
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206
247
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(Rel.
(Rel.
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Conservative 0;
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041; C_TYPE_LECTIN_2; 1.
Calcium; Surface film; Gaseous
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                                               STANDARD;
                                                                                                                                                                                                                                                                                                                         Collagen;
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TISSUE=Lung;
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40,
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245
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237
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206
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                                                                                                                                 54
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Chordata;
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Last sequence update)
Last annotation update)
                          Created)
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                                                                                                                                                                                                                                                                                                                        Repeat.
                                                                                                                                                     ; Score 10; DB
k; Pred. No. 0.3
0; Mismatches
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C-TYPE LECTIN
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCN)
                                                                                                                                                                                                                                                                                                 POTENTIAL.
PULMONARY
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                                               247
                                                                                                                                                                                                                  (GLCNAC.
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                                                                                                                                                                                                                                                                                              SURFACTANT-ASSOCIATED PROTEIN
                                                                                                                                                                  DB 1;
0.35;
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A Chen Q., Boggaram V., Mendelson C.R.;

"Rabbit lung surfactant protein A gene; identification of a lung-
ty specific Duase I hypersensitive site.";

Am. J. Physiol. 262:1662-1671(1992).

"C. I. FUNCTION: IN PRESENCE OF CALCIUM IONS, PSAP BINDS TO SURFACTANT
C. PHOSPHOLIPIDS AND CONTRIBUTES TO LOWER THE SURFACE TENSION AT THE
C. AIR-LIQUID INTERFACE IN THE ALVEOLI OF THE MAMMALIAN LUNG AND IS
C. ESSENTIAL FOR NORMAL RESPIRATION.
C. SUBUNIT: OLIGOMERIC COMPLEX OF 6 SET OF HOMOTRIMERS.
C. SUBUNIT: OLIGOMERIC COMPLEX OF 6 SET OF HOMOTRIMERS.
C. SUBUNIT: OLIGOMERIC COMPLEX OF 6 SET OF HOMOTRIMERS.
C. SUBUNIT: OLIGOMERIC COMPLEX OF 6 SET OF HOMOTRIMERS.
C. I. SUBUNIT: OLIGOMERIC SUBPACTANT CONSISTS OF 90% LIPID AND 10%
PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS
PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS
C. CARBOHYDRATE-BINDING GLYCOPROTEIN SSOCIATED PROTEIN: 2 COLLAGENOUS
C. I. SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
C. I. SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                          Query Match
Best Local :
          Matches
                                                                                 VARIANT
CONFLICT
SEQUENCE
                                                                                                                                           DOMAIN
DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                Signal;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A29931; LNRBPS
HSSP; P22897; 1EGG.
InterPro; IPR000087; C
InterPro; IPR001304; I
                                                                                                                                                                                                                                                                                                          PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Calcium; Surface film; Gaseous
                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00059; lectin c; 1.
Pfam; PF00059; lectin c; 1.
Pfam; PF01391; Collagen; 2.
SMART; SM00034; CLECT; 1.
PROSITE; PS000615
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                                                                                                                                                                                                                                                             CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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MEDLINE=92312742; PubMed=1616051;
Chen Q., Boggaram V., Mendelson C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88139348; PubMed=2830270;
Boggaram V., Qing K., Mendelson C.R.;
Brimary sequence and cyclic AMP and developmental regulation.";
J. Biol. Chem. 263:2939-2947(1988).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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SFTPA1 OR SFTPA
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                          Similarity
                                                                                                                                                                                                                                                                                              Lectin;
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        Conservative
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S -> P.
GPMG -> APWA (IN RE)
W; 289634054CBC8CB4 (
    0;
                    Score 10;
Pred. No.
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C-TYPE LECTIN
BY SIMILARITY.
BY SIMILARITY.
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PULMONARY
        Mismatches
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                    DB 1;
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2 COLLAGENOUS,
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RESULT 13
PSPA_CANFA
                                                                                             Glycoprotein;
Signal; Lectin
SIGNAL
              DISULFID
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                                        DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structure of canine pulmonary surfactant apoprotein: cDNA and complete amino acid sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSPA.
                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1988 (Rel. 06, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-04T-2001 (Rel. 40, Last annotation update)
Pulmonary surfactant-associated protein A pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P06908;
                                                                                                                                                                 Pfam; PF00059; lectin_c; 1.
Pfam; PF01391; Collagen; 2.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                 EMBL; M11769; AAA30887.1;
                                                                                                                                                                                                                                                                                           or send an
                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patthy L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=87115834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C-TYPE LECTIN DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     White R.T
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                                                                                  CHAIN
                                                                                                                        PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Calcium; Surface film;
                                                                                                                                                                                                                                     HSSP; P22897; 1EGG
                                                                                                                                                                                                                                                 PIR; A25296; LNDGPS.
 CARBOHYD
                                                                                                                                                                                                     InterPro; IPR000087; Collagen.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Is lung surfactant protein a lectin-collagen hybrid?";
lature 325:490-490(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: OLICOWIBALE COLL.
SUBCELLULAR LOCATION: Extracellular.
SUBCELLANEAR LOCATION: Extracellular.
MISCELLANEOUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND 10%
PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS,
PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS,
PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: IN PRESENCE OF CALCIUM IONS, PSAP BINDS TO SURFACTANT PHOSPHOLIPIDS AND CONTRIBUTES TO LOWER THE SURFACE TENSION AT THAT ALVEOLI OF THE MAMMALIAN LUNG AND IS ESSENTIAL FOR NORMAL RESPIRATION.

SUBUNIT: OLIGOMERIC COMPLEX OF 6 SET OF HOMOTRIMERS.
                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) HYDROPHOBIC PROTEINS (SP-B AND SP-C).
SIMILARITY: CONTAINS A COLLAGENUS DOMAIN.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute.
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155
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                                                                                               Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sci.
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PubMed=3863100;
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C-TYPE LECTIN (
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNA
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COLLAGEN-LIKE
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                                          FORM).
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  (POTENTIAL).
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Best Local S
Matches 10
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P07714;
01-APR-1988
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                        "Characterization of a second human pulmonary surfactant-associated
protein SP-A gene.";
bm .T name.
                                                                                                                                                                                                                                                                                                                                                                                                                                     apoprotein
Nature 317:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=86250832; PubMed=3755136;
Floros J., Steinbrink R., Jacobs K., Phelp
Sultzman L., Jones S., Taeusch H.W., Frank
"Isolation and characterization of cDNA cl
pulmonary surfactant-associated protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=86250832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                associated protein).
SFTPA1 OR SFTPA OR SFTP1
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01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
                                       use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=86014366; PubM
White R.T., Damm D., M
Benson B., Cordell B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pulmonary surfactant-associated protein A precursor (SP-A) (PSP-A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
EMBL; M13686;
EMBL; K03475;
                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                 the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Isolation and characterization of the human pulmonary surfactant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PSAP) (Alveolar proteinosis protein) (35 kDa pulmonary surfactant-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol.
                                                                                                                                                      PHOSPHOLIPIDS AND CONTRIBUTES TO LOWER THE SURFACE TENSION AT THE ALVEOLI OF THE MAMMALIAN LUNG AND IS AIR-LIQUID INTERPACE IN THE ALVEOLI OF THE MAMMALIAN LUNG AND IS ESSENTIAL FOR NORMAL RESPIRATION.

SUBCRITI: OLIGOMERIC COMPLEX OF 6 SET OF HOMOTRIMERS.

SUBCRILIULAR LOCATION: Extracellular.

MISCELLANEOUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND 10% PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS, CARROHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL HYDROPHOBIC PROTEINS (SP-B AND SP-C).

SIMILARITY: CONTAINS A COLLAGENOUS DOMAIN.
                                                                                                                                                                                                                                                                                                                      J. Respir. Cell Mol. Biol. 6:446-452(1 FUNCTION: IN PRESENCE OF CALCIUM IONS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 GLPGRDGRDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                      tein gene.";
317:361-363(1985)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chem. 261:9029-9033(1986).
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248 AA;
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 AAA60211.1;
AAA36520.1;
                                                                                                                                                                                                                                                                                                                                    Cell Mol. Biol. 6:446-452(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=2995821;
D., Miller J., Spratt K.,
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Frank H.A., Fritsch
NA clones for the 39
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                                                         oved. Usage by and for commercial (See http://www.isb-sib.ch/announce)
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6 outstation -
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Best Local
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P35242;
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EMBL; M68519; AAA6031:
PIR; A24622; LNHUPS.
PIR; A25720; LNHUP6.
PIR; B25720; LNHUP1.
HSSP; P22897; 1EGG.
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VARIANT
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Signal; Lectin
SIGNAL
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PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
Glycoprotein; Calcium; Surface film; Gaseous
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InterPro; IPR001304; Lectin_C.
Pfam; PF00059; Lectin_C: 1.
Pfam; PF01391; Collagen; 2.
SMART; SM00034; CLECT; 1.
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 NCBI_TaxID=10090;
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; J
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                             Mus musculus (Mouse)
                                                             SFTPA1 OR SFTPA OR SFTP1
                                                                                           Pulmonary
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HGNC:10798; SFTPA1.
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surfactant-associated protein A p
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AAA60319.1;
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MGD; MGI:109518; Sftpa.
InterPro; IPR000087; Collagen.
InterPro; IPR01304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
Pfam; PF01391; Collagen; 2.
SMART; SM00034; CLECT; 1.
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DOMAIN
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CARBOHYD
SEQUENCE
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SIGNAL
CHAIN
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PHOSPHOLIPIDS AND CONTRIBUTES TO LOWER THE SURFACE TENSION AT THE PHOSPHOLIPIDS AND CONTRIBUTES TO LOWER THE MAMMALIAN LUNG AND IS ESSENTIAL FOR NORMAL RESPIRATION.

PESSENTIAL FOR NORMAL RESPIRATION.

SUBUNIT: OLIGOMERIC COMPLEX OF 6 SET OF HOMOTRIMERS.

SUBUNIT: OLIGOMERIC COMPLEX OF 6 SET OF HOMOTRIMERS.

SUBCELLULAR LOCATION: EXCLEDED PROTEIN: 2 COLLAGENOUS, PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS,
                                                                                                                                                                                                                                          PROSITE; PS00615; C_TYE
PROSITE; PS50041; C_TYE
Glycoprotein; Calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                      EMBL; S48768;
PIR; A48853; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93072386; PubMed=1443158;
Korfhagen T.R., Bruno M.D., Glasser S.W., Ciraolo
Lattier D.L., Wikenheiser K.A., Clark J.C.;
"Murine pulmonary surfactant SP-A gene: cloning,
                                                                                                                                                                                                                                                                                                                                                                                                           or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D)
HYDROPHOBIC PROTEINS (SP-B AND SP-C)
-i- SIMILARITY; CONTAINS A COLLAGENOUS DOMAIN.
-i- SIMILARITY; CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=DBA/2J;
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GLPGRDGRDG
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TYPE LECTIN 2; 1.
TYPE LECTIN 2; 1.
um; Surface film; Gaseous
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BY SIMILARITY.
BY SIMILARITY.
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N-LINKED (GLCNAC. . .) (
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Pred. No.
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Search completed: June 20, 2003, 11:41:18 Job time : 18 secs

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243
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sp_phage:*
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O9n1x4 sus scrofa
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O57451 gallus gall
O9i9q7 carassius a
O9tt06 ovis aries
O9n0g1 equus cabal
O95188 equus cabal
O95188 equus cabal
O95qq1 mus musculu
O98ta4 gallus gall
O9i9q cyprinus ca
O8wp36 suberites d
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Q9ucj3 homo sapien
Q19813 caenorhabdi
Q9acn2 streptococc
Q8tcd8 homo sapien
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	170	164	149	149	111	109	107	87	52	46	2315	2288	1752	763	751	695	684	589	567	441	260	260	182	1940	1761	812	694	447	358
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	Q9GLV5	P74713	Q9JWV2	09ЛХВ1	Q9RD99	Q9CVJ2	Q9BQY7	Q45313	Q9HZ09	Q63074	Q95ZK3	Q23081	Q07265	Q61482	Q60709	Q64348	P90679	Q9AK64	Q9SWQ3	Q90YI9	Q9QXU9	Q9UHG2	Q9CYS4	29VMV5	018407	Q06452	Q97T45	Q9YTJ3	Q9J3U4
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ALIGNMENTS

유 성	Qu Be Qy Db	SO KW	R R R R R R R R R R R R R R R R R R R	Q8R002 ID Q AC Q
242 FA 243 	Query Match 25.5%; Score 62; DB 11; Length 243; Best Local Similarity 100.0%; Pred. No. 4.8e-52; Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 182 FGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSPV 241	SEQUENCE FROM N.A. SEQUENCE FROM N.A. Strausberg R.; Sthausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC023066; AAH23068.1; EMBL; BC025174; AAH25174.1; EMBL; BC025174; AAH25174.1; Hypothetical protein. SEQUENCE 243 AA; 25420 MW; 498129CD051DB97B CRC64;	01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Similar to DKFZP586B0621 protein (Hypothetical 25.4 kDa protein). Mus musculus (Mouse). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Buharyota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI TaxID=10090; [1]	BRO02 PRELIMINARY; PR' BRO02; 1-JUN-2002 (TrEMBLrel. 21, Creat

PRELIMINARY;

PRT;

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Q9UCJ3
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Q9UCJ3;
01-MAY-2000
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SEQUENCE
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STRAIN-BRISTOL N2;
Wilson R., Bentley D., Gattu
"The sequence of C. elegans
Submitted (APR-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteinosis.";
Am. J. Pathol. 142:241-248(1993).
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MEDLINE=99069613;
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NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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01-NOV-1996 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Mammalia; Eutheria; Primates;
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01-JUN-2001
                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                         Submitted
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STRAIN=BRISTOL N2;
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                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                           InterPro;
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                                                                                                                  Pro; IPR002486; Col_cuticle_N.
PP01391; Collagen; 3.
PP01484; Col_cuticle_N; 1.
QCE 289 AA; 28740 MW; DFFB
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l Similarity
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27 AA; 2696 MW; 8
                                                                                                                                                                                                                                                                                            (JUN-1999) to the EMBL/GenBank/DDBJ
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O (TrEMBLrel. 13,
L (TrEMBLrel. 17,
clarity 100.0%; I
Conservative 0;
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                                                       4.5%;
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egans cosmid F26F12.";
o the EMBL/GenBank/DDBJ
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21,
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Last sequence update)
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red. No. 0.0
Mismatches
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RESULT
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Matches 11
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01-JUN-2002
01-JUN-2002
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STRAIN=655;
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                                                                                                                                 EMBL; BC022318; AAH22318.1; -. Hypothetical protein. SEQUENCE 375 AA; 37655 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane.
SEQUENCE 306
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Pfam; PF00746; Gram pos anchor; 1.
PRINTS; PR00015; GPOSANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Streptococcus pyogenes sclB er protein with a collagen-like re Microbiology 147-419-429 (2001).
EMBL; AJ301809; CAC33778.1; -.
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01-JUN-2002
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PROSITE; PS00343; GRAM_POS_ANCHORING;
                                                                                                                                                                                            Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                    Hypothetical 37.7 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002
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                                                                                                                                                                                                                                     FISSUE=LUNG
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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InterPro; IPR001899; Gram pos_anchor.
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GLPGRDGRDGR 55
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                                                         Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31833 MW;
                                                                                                                                                                                                                                                                                                               Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91
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Pred. No. 0.0
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57EBDC244DF17600 CRC64;
                                                                                                                                       CCB7375D3C86421A CRC64;
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0.027;
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0.033;
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Best Local
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SEQUENCE
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SIGNAL
                                                                                                                                                                                                                                                                                                             01-JUL-1997 (TrEMBLrel. 04, Create 01-JUL-1997 (TrEMBLrel. 04, Last s; 01-JUN-2002 (TrEMBLrel. 21, Last a; 01-JUN-2002 (TremBLrel. 21, Last a; Surfactant protein A2 (Fragment). Papio cynocephalus (Yellow baboon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pfam; PF01391; Collagen; 3.
pfam; PF00059; lectin c; 1.
ProDom; PF000007; Collagen; 2.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9N1X4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=20109098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fung
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01-OCT-2000
                                                                                                                                                                                                                                  NCBI_
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Immunol. 164:1442-1450(2000).
EMBL; AF132496; AAF22145.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002
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  Gao E., Wang Y., McCormick & Submitted (MAY-1997) to the
                                      TISSUE=KIDNEY;
                                                         SEQUENCE FROM N.A.
                                                                                             MEDLINE=97053398; PubMed=8897910; Gao E., Wang Y., McCormick S.M., Li J., Sei "Characterization of two baboon surfactant Am. J. Physiol. 271:L617-L630(1996).
                                                                                                                                                                             TISSUE=KIDNEY
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P35247; 1B08.
InterPro; IPR000087; Collagen.
InterPro; IPR001304; Lectin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Porcine Lung Surfactant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        localisation and tissue distribution.
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CT-2000 (TrEMBLrel. 15, Last sec
DM-2002 (TrEMBLrel. 21, Last and
Burfactant protein D precursor.
                                                                                                                                                                                                                                    TaxID=9556;
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Butheria;
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sman H.P., Skinner
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378 I
37986 MW;
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Cetartiodactyla; Suina;
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TYPE_LECTIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.5%;
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  S.M., Li J., Seidner
e EMBL/GenBank/DDBJ di
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                              Created)
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Pred. No.
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LUNG SURFACTANT PROTEIN
3504E8C1E56C341D CRC64
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                                                                                                                                                                                                                                                                          Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                 sequence update)
annotation update)
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0.033;
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ina; Suidae;
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i; Cercopithecidae;
                                                                                                                  Seidner S.R., Mendelson C.R.; ant protein A genes.";
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  er S.R., Me
databases.
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Sus.
                                                                                                                                                                                                                                                                                             Euteleostomi;
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                    Mendelson
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RESULT 9
Q91907
ID Q919
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AC Q919
OT 01-C
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GN MBL.
OS Cara
OC Buka
OC Cypt
OX NCBL
RN [1]
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057451
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Matches 10
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Best Local
                                                                 Q919Q7 PRELIMINARY;
Q919Q7;
01-OCT-2000 (TrEMBLrel. 15, C:
01-OCT-2000 (TrEMBLrel. 15, L:
01-JUN-2002 (TrEMBLrel. 21, L:
Mannose binding-like lectin p
                                                                                                                                                                                                                                                                                                                                            Laursen S.B.;
Submitted (AUG-1997) to the EMBL Submitted (AUG-1997) to the EMBL EMBL; AF022226; AAB94071.1; -. HSSP; P19999; 1YTT.
InterPro; IPR001087; Collagen.
InterPro; IPR001304; Lectin C.
Carassius auratus (Goldfish).
Bukaryota; Metazoa; Chordata; C
Actinopterygii; Neopterygii; Te
Cyprinidae; Carassius.
NCBI TaxID=7957;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom;
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NON TER
SEQUENCE
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EMBL; AF003896; AAB61
InterPro; IPR000087;
                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                             MBL.
                                                                                                                                                                                                                                                                                                    ProDom; PD000007; Collagen; 1.
SMART; SM00034; CLECT; 1.
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                                                                                                                                                                                                                                                                                                                           Pfam; PF00059; lectin_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CMBL
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57 57
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238 1
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Conservative
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AAB61294.1;
                                                                                                                                                                                                                                                                                  C_TYPE_LECTIN_1;
C_TYPE_LECTIN_2;
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25645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.1%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49
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                                                                                                                                                                                                                                   4.1%;
                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=LIVER;
                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                ; Score 10; DB
%; Pred. No. 0.2
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ
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                                                                    Last sequence update)
Last annotation update)
precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 10;
Pred. No.
                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B25149EC822F643C CRC64;
                              Craniata;
Teleostei;
                                                                                                                                                                                                                                                        E5C9B5197AAE64E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                    UNKNOWN_1.
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                              Vertebrata; Euteleostomi;
Ostariophysi; Cypriniform
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                                                                                                                                                                                                                                    13;
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TISSUE=LIVER;

SEQUENCE FROM

N.A.

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Best Local S
Matches 10
                                                                                                                                                                                          Braems G.A., Yao L.-J., Inchley K., Brickenden & Grolla A., Challis J.R.G., Possmayer P.; "Ovine surfactant protein cDNAs: use in studies and maturation after prolonged hypoxemia."; Am. J. Physiol. 278:L754-L764(2000).
  PROSITE;
                                                                                     Am. J. Physiol. 278:L765-L778(2000)
EMBL; AF211856; AAF18995.1; -.
EMBL; AF076633; AAF31148.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                               Q9TT06;
                      Pfam; PF01391; Collagen; 2. Pfam; PF00059; lectin c; 1. SMART; SM00034; CLECT; 1.
                                                                                                                      Pietschmann S.M., Pison U.;
"CDNA cloning of ovine pulmonary SP-A,
two different sequences for SP-B.";
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
Bovidae; Caprinae;
                                                    HSSP; P22897; 1EGG.
InterPro; IPR000087; Collagen.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=LUNG;
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=20215262; PubMed=10749753;
                                                                                                                                                                                                                                                                                                                                   Ovis aries (Sheep)
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                                                                                                                                                                                                                                                                                                                                                                  Pulmonary surfactant protein
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                        MEDLINE=20215263;
                                                                                                                                                                                                                                                                                                                                                         protein A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01391; Collagen; 2.
Pfam; PF00059; lectin c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenetics 51:955-964(2000).
EMBL; AF227739; AAF63470.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      structure predicts affinity for galactose.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Witved L., Holmskov U., Koch C., Teisner "The homologue of mannose-binding lectin is expressed at high level in spleen, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20456722; PubMed=11003389;
Vitved L., Holmskov U., Koch C., T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inte#Pro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P35247; 1B08.
Pro; IPR000087; Collagen.
Pro; IPR001304; Lectin_C.
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PS50041; C_TYPE_LECTIN_2; 1.
             PS00615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLPGRDGRDG
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246 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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13
145
25709 }
C_TYPE_LECTIN_1;
C_TYPE_LECTIN_2;
                                                                                                                                                      PubMed=10749754;
                                                                                                                                                                                                                                                                                                    Ovis.
                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebra
Cetartiodactyla; Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44
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100.0%;
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Last annotation update)
n A (Pulmonary surfactant-associated
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S -> F.
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Pred. No.
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                                                                                                                                                                                                                                          Brickenden A.,
                                                                                                                                                                                                                                                                                                                                                                                                                        248
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                                                                                                                                  SP-B,
                                                                                                                                                                                                                                                                                                          Vertebrata; Euteleostomi;
minantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13; Length 246; 0.21;
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the carp fa
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                                                                                                                                  SP-C:
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                                                                                                                                                                                                                   fetal lung growth
                                                                                                                                                                                                                                           Han V.K.M.,
                                                                                                                                 isolation
                                                                                                                                                                                                                                                                                                            Bovoidea;
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Q9N0G1
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Best Local S
Matches 10
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Best Local S
Matches 10
                                                                                                       Weber B.I.L., Hospes R., Gortne
Submitted (JUL-2001) to the EME
EMBL; AP400580; AAL07690.1; -
InterPro; IPR001087; Collagen.
InterPro; IPR001304; Lectin C.
                                                                                                                                                                                                                                                                                                                                                                        Q95L88; PRELIMINARY; PRT; 248 AA.
Q95L88; O1-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLER). 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-1998) to the EMBL; AB015963; BAA97976.1; HSSP; P35247; 1B08.
                         PROSITE; PS00615; C
                                                                    Pfam; PF01391; Collagen; 2. Pfam; PF00059; lectin_c; 1.
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                          Pulmonary surfactant-associated protein
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InterPro; IPR001304; Lectin_C.
Pfam; PF001391; Collagen; 2.
Pfam; PF00059; lectin_C; 1.
SMART; SN00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=THOROUGHBRED; TISSUE=LUNG
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                           Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning of equine pulmonary surfactant proteins.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9796;
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PS50041; C_TYPE_LECTIN_2; 1.
248 AA; 26000 MW; BBE12EFB05C2B8D1 CRC64;
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_TYPB_LECTIN_1; UNKNOWN_1.
_TYPB_LECTIN_2; 1.
_26047 MW; B71133E005C9A5C1
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100.0%; Pr
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Perissodactyla; Equidae; Equus.
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4.
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Perissodactyla; Equidae; Equus.
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Pred. No.
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Pred. No.
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0.21;
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CRC64;

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RESULT 13
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RESULT 14
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A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Ksukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Marchia R., Vochida K., Hasecawa Y., Kawaii H., Kohtsuki S.,

Vochida K., Hasecawa Y., Kawaii H., Kohtsuki S.,
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Best Local (
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01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AK011333; BAB27551.1; -.
EMBL; AK004620; BAB23416.1; -.
EMBL; AK004788; BAB23565.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=2108566Q; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=EMBRYO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Surfactant associated protein
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01-JUN-2002 (TrEMBLrel.
  Q98TA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wynshaw-Boris A., Yoshida K., Hasegawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000087; Collagen.
InterPro; IPR001304; Lectin_C.
Pfam; PF01391; Collagen; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Functional annotation of a full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:109518;
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                                                                                                                                                                                                                                                                                                                                                                                                                            PF01391; Collagen; 2. PF00059; lectin_c; 1.
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Similarity 100.0%;
10; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                  SM00034; CLECT;
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                                                                                                                                                                                                                                                                                                                          PS00615; C_TYPE_LECTIN_1;
PS50041; C_TYPE_LECTIN_2;
248 AA; 26183 MW; 8A56
                                                                                                                                                                        GLPGRDGRDG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shinagawa A., Shibata K.,
                                                                                                                            GLPGRDGRDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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     PRELIMINARY;
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Rodentia;
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                                                                                                                            49
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                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                           4.1%;
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17,
21,
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in A.
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                                                                                                                                                                                                                                                      Score 10;
Pred. No.
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Sciurognathi; Muridae; Murinae; Mus
     PRT;
                                                                                                                                                                                                                                                                                                                               BA5670CFAD3EB9B6 CRC64;
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Konno H., Adachi J., Fukuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248
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0.21;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               991909;
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                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lectin;
                                                                                                                                                                                                                                                                                TISSUE=LIVER;
                                 InterPro;
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                      [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47
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          IPR000087; Collagen.
IPR001304; Lectin_C.
1391; Collagen; 2.
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254
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=20456722; PubMed=11003389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mannose-binding lectin protein precursor. Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01391; Collagen; 1.
Pfam; PF00059; lectin c; 1.
ProDom; PD000007; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
MEDIINE=20456722; PubMed=11003389;
Vitved L., Holmskov U., Koch C., Teisner B., Hansen S.,
Vitved L., Holmskov U., Koch C., Teisner B., Hansen S.,
"The homologue of mannose-binding lectin in the carp fam
is expressed at high level in spleen, and the deduced pr
structure predicts affinity for galactose.";
Immunogenetics 51:955-964(2000).
EMBL; AF227737; AAF63468.1; -.
HSSP; P35247; 1808.
                                                                                                                                                                                                                                                    Cyprinus carpio (Common carp)
Eukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii;
Cyprinidae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21, Mannose binding-like lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000005; HTHAraC.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000087; Collagen.
InterPro; IPR000005; HTHAraC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenetics 51:955-964(2000).

3MBL; AF231714; AAK30298.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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254 M
234 D
27376 MW;
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MANNOSE-BINDING LECTIN
D -> V.
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Pred. No.
                                                                                                                                                                                                                                                                            Craniata;
Teleostei;
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                                                                                                                                                                                                                                                                                                                                                                               sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256
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0.21;
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mes; Phasianidae; Phasiani
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Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hansen S., baya
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he carp family Cyprinidae
deduced primary
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                                                                                    S., Skjodt K.;
family Cyprinidae
d primary
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DR Pfam; PF00059; lectin_c; 1.

DR SMART; SM00034; C_TYPE_LECTIN_1; UNKNOWN_1.

DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

KW Lectin; Signal.

FT SIGNAL 1 23 POTENTIAL.

FT CHAIN 24 256 MANNOSE BINDING-LIKE LECTIN.

FT CHAIN 235 , 235 S -> T.

SQ SEQUENCE 256 AA; 26934 MM; D019291D1167730D CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 0.22;

Matches 10; Conservative 0; Mismatches 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Gaps 0;

Search completed: June 20, 2003, 11:42:03

Search completed: June 20, 2003, 11:42:03
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                       Score
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seq length: 2000000000
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1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*

5: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*

7: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*

7: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*

8: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
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1 MRPLLVLLLLGLAAGSPPLD......DSTESGFLVYSDWHSSPVFA 243
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Copyright (c) 1993 - 2003 Compu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT: *
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT: *
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       AAY06481

AAY17827

AAW917924

AAB33461

AAY71468

AAY93688

AAW93688

AAW931318

AAW65815

AAB65815
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Peptide
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44423.5
44233.5
44242.5
5.0.2
6.0.2
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		AAB49598	22	244	32.0	#2
Human ACRP30 prote		AAB49592	22	244	•	#2
Human adipocyte co		AAB65828	22	244	32.0	#2
Human OBG3 protein		AAE05529	22	244	32.0	**2
(Adip		AAY71035	21	244	٠	#2
dipod		AAB30233	21	244		#2
se most		AAY21807	20	244	32.0	#2
Mouse adipoQ prote		ABB08221	23	247	٠	vi
Mouse OBG3 protein		AAE05527	22	247	٠	U
Human adipocyte co		AAW09108	18	244	32.1	U
Mouse acrp30 prote		ABB08222	23	247	32.7	UI
Mouse OBG3 protein		AAE05528	22	247	32.7	U
Murine adipocyte c		AAW09107	18	247	32.7	U
		ABB80582	23	333	•	vi
sbg103		ABB80583	23	225	33.9	Uī
Novel human diagno		ABG12723	22	151	٠	ω
e TANGO		AAB65824	22	128	49.1	O
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Human adipocyte co		AAB49599	22	243	100.0	01

20-NOV-1998; 05-JAN-1998; 29-APR-1998; Human tumour-associated protein PRO344. AAY06481 standard; Protein; 243 PRO344; UNQ303; cancer; tumour; diagnosis; therapy; human. 27-SEP-1999 (first entry) 98US-0109304. 98US-0070440. 98US-0083500. 99WO-US00106 /note= "N-myristoylated"
216..243
/note= "N-myristoylated" 68..215 /note= "signal peptide" 16..243 /note= "mature Location/Qualifiers protein" ALIGNMENTS B

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RESULT 2
AAY17827
ID AAY1
XX
AC AAY1
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DT 12-A
XX
DE Huma
XX
KW Huma
KW Secr
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OS Homo
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents human PRO344 (UNQ303), a protein encoded by the novel cDNA clone DNA40592 (see AAX87258). Amplification of DNA40592 was observed in primary lung tumours and in primary colon tumours, suggesting a significant role in tumour formation and growth. Antagonists (e.g. antibodies) directed to PRO344 may have use in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour cells. Such amplification is expected to be associated with overexpression of the gene product and to contribute to tumorigenesis. The encoded proteins (see AAX06477-90) may be useful targets for the diagnosis and/or treatment (including prevention) of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAY-1998;
10-JUN-1998;
10-NOV-1998;
                            Human; PRO protein; tumour necrosis factor family; TNF; cytokine; secreted protein; transmembrane protein; inflammation disorder.
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                                                                          Human
                                                                                                      12-AUG-1999
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N-PSDB; AAX87258.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bind the proteins are claimed and used in claimed cancer nostic kits.
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243; Conserv
                                                                          PRO344
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                                                                                                                                                                                                                                                             VFA 243
                                                                                                                                                                                                                                                                                                      FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
                                                                                                                                                                                                                                                                                                                                              APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
                                                                                                                                                                                                                                                                                                                                                                                                       APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                                                                                                                                                                                                                                                                                                                                              APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
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Ood
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 AA;
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                                                                       protein
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98US-0088742.
98US-0107783.
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16-DEC-1997;
16-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic, anti-inflammatory, anti-proliferative and immu
activity. The proteins and polynucleotides can be used in
identification of homologues, raising antibodies and design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes nucleic acids encoding PRO secreted transmembrane proteins used therapeutically. The PRO proteins have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding PRO secreted and transmembrane proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
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17-DEC-1997
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                                                                                                                                                                                                                                                                                    1 MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                   APLPFDRVLVNEQGHYDAVTGKPTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
                                                                                                                                                                                                                                              APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                                                                                                                                                                                                                   MRPLLVLLLIGLAAGS PPLDDNKI PSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGRPG
                                                       VFA
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                                                                                                                                FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
                                                                                                                                                                    APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
                                                                                                                                                                                                                            APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
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                                                                                                                                                                                                                                                                                                                                              Conservative
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97US-0069870.
97US-0069873.
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98US-0074092
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97US-0069696
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97US-0069425.
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                                                                                                                                                                                                                                                                                                                                           Score 1325; DB 20;
Pred. No. 5.3e-103;
D; Mismatches 0;
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180 180 120 120 60 60

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This polypeptide comprises human adipocyte-specific protein zsig39, a protein that modulates free fatty acid metabolism. zsig39 is a member of a family of proteins having a globular domain and a collagen-like domain capable of dimerisation or oligomerisation. zsig39 polypeptides were initially identified by querying an EST
                                                        Claim
                                                                                                              Humes
                                                                                                                                              26-AUG-1997;
                                                                                                                                                             26-AUG-1998;
                                                                                                                                                                              04-MAR-1999
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secretory signal
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                                                                                                                                                                                                                                                                                            "beta
                                                                                                                                                                                                                                                                                                                                                                                          "globular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                         "mature protein, alternatively the protein comprises residues 19..24; (specifically claimed in Claim 4)
                                                                                                                                                                                                                                             "beta
                                                                                                                                                                                                                                                            "beta
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antimicrobial.
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ially identified by querying an EST sequences characterised by an upst
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                                                                     acid metabolism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           methionine start site, a hydrophobic region of approximately 13 cd amino acids and a cleavage site. A single EST sequence was discovered, and the novel polypeptide encoded by the full-length CDNA allowed the identification of a homologue relationship with adipocyte complement related protein Acrp30 and adipocyte secreted protein apM1. A full-length clone (see AAX24684) was obtained from a lung tissue library. Expression vectors, cultured cells and a method of producing zsig39 polypeptide are claimed, as well as complement related protein affinity tags, toxins, radionucleotides, enzymes or fluorophores, fusion proteins including zsig39 polypeptides, an antibody that specifically binds to an epitope of zsig39, and a method for modulating free fatty acid metabolism by administering a zsig39 polypeptide. The czsig39 polypeptide may also be used in organ preservation, for cryopreservation, for surgical pretreatment to prevent injury due to ischaemia and/or inflammation, and as an antimicrobial agent, recomplement in production and a polypeptide or phagocytosis of infectious agents.
                                                                                                                                                                                                                                                                                                                                                                               Matches 243;
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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VFA
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                                                                     FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
                                                                                             FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
                                                                                                                                               APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
                                                                                                                                                                                 APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
                                                                                                                                                                                                                                                                                                   MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
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                                 243
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Pred. No. 5.3e-103;
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AAB33461 RESULT 4

AAB33461 standard; Protein; 243

AAB33461;

29-JAN-2001 (first entry)

Human PRO344 protein UNQ303 SEQ ID NO:241.

haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective; antianaemic; hepatotropic; virucide; antiporniatic; antiallergic; antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; apondyloarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune thrombocytopaenia; immune-mediated renal disease; demyelinating disease; hepatobiliary disease; Whipple's disease; inflammatory bound disease; autoimmune disease; inflammatory dermatological; antiarthritic; Homo sapiens immunological rejection; immune related disease; diagnosis; bowel disease; gluten-sensitive enteropathy; isease; immune-mediated skin disease; allergic disease; disease; transplantation associated antirheumatic; immunosuppressive antiinflammatory; cardiant; disease; diabetes mellitus; disease;

used

Indels Length

Gaps

60 0

180

120 60

120

240 180

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243; 0;

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be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematous, rheumatoid arthritis, escleroarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Systemic sclerosis, idiopathic, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaemia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases,
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01-DEC-1999;
01-DEC-1999;
02-DEC-1999;
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29-OCT-1999;
29-NOV-1999;
30-NOV-1999;
                                                                                                                                                                                                                                              Sixty four PRO polypeptides, useful in the diagnosis and treatment immune related disorders, e.g. systemic lupus erythematosis, rheumarthritis, osteoarthritis, thyroiditis and diabetes mellitus -
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02-DEC-1999
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28-JUL-1999,
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Kabakoff RC,
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14-MAY-1999;
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99WO-US31274

2000WO-US00219

2000WO-US00277

2000WO-US00376

2000WO-US03565

2000WO-US04341

2000WO-US04341

2000WO-US044414
                                                                                                                                                                                                                                                                                                                                                    Tumas
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                                                                                                                                                                                                                   96; 309pp; English.
                                                                                                                                                                                                                                                                                                                                                                  Lu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US28551.
99WO-US28564.
99WO-US28565.
99WO-US30095.
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99WO-US28301.
99WO-US28634.
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99US-0162506.
99WO-US28214.
99WO-US28313.
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99US-0146222.
99WO-US20111.
99WO-US20594.
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Lu Y, Pan J,
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99WO-US08615.
99US-0131445.
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99WO-US21547.
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99US-0125775
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-0134287.
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J, Pennica D, Shelto
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Best Local Sim
Matches 243;
            01-DEC-1998;
                                      30-NOV-1999;
                                                                                                                                                                       Binding-site
                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                          PRO344; DNA40592-1242; human; ATCC No: 209492; antiproliferative; meoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour; breast; prostate; colon; lung; renal; ovarian; central nervous system; CNS; leukemia; melanoma; Expressed Sequence Tag; EST; secreted protein; CNS; leukemia; melanoma; Expressed Sequence Tag; EST; secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-NOV-2000
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                                                                   08-JUN-2000.
                                                                                                WO200032778-A2
                                                                                                                                           Modified-site
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                                                                                                                                                                                                                                 Protein
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                                                                                                                                                                                                                                                                                                                                                              domain;
            98WO-US25108
                                       99WO-US28409
                                                                                                                                           /note= "(
216..222
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77..80
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/label= Mature_PRO344_protein
                                                                                                                                                                                                                                                             /label= Signal_peptide
11...17
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                            note= "N-myristoylation site"
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Pred. No. 5.3e-103;
Mismatches 0;
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Claim

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Best Local S
Matches 243
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22-DEC-1998;
20-JUL-1999;
                                                                     PRO201;
PRO715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the human PRO344 protein, encoded by the cDNA clone, designated as DNA40592-1242. It is isolated from human foetal lung tissue, cDNA library, identified using probes based on a consensus sequence DNA34398, derived from secreted protein extracellular domain (ECD) expressed sequence tag (EST). This clone is assigned ATCC deposit No: 209492. PRO344 functions as a nephastic cell growth inhibitor and the process of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition useful for inhibiting neoplastic cell growth and treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide their antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is used for treating tumours, using an effective amount of PRO655, and PRO344. This composition is especially useful for treatment of cancers such as breast, prostate, colon, lung, renal, ovarian and leukemia and melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 31;
                            Homo
                                                    tumourigenesis;
                                                                                                               Amino
                                                                                                                                          03-OCT-2000
                                                                                                                                                                       AAY93688;
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                                                    PRO292; PRO327; PRO1265; E
PRO1017; PRO1112; PRO509; E
genesis; cancer; neoplastic
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                                                                                                                                                                                                  standard;
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|llarity 100.0%; |
|Conservative 0;
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98US-0113296.
99US-0144758.
99US-0145698.
Location/Qualifiers
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                                                                                                           polypeptide PRO344.
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Pred. No. 5.3e-103;
; Mismatches 0;
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                                                    PRO344; PRO343; PRO347; PRO357;
PRO853; PRO882; tumour cell;
c cell growth; cell proliferation
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01-SEP-1999;
15-SEP-1999;
30-NOV-1999;
30-NOV-1999;
01-DEC-1999;
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N-PSDB;
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08-MAR-1999;
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                                                                                                                                                                                                                                                                                                                              proliferation
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DB; AAA46907.
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            APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
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99WO-US05028.
99WO-US12252.
99WO-US20111.
99WO-US21090.
99WO-US28313.
99WO-US28301.
99WO-US28301.
                                                                                                                                                                                                                                                                                                   A,
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216..2
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/note=
11..17
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77..80
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The present sequence represents a novel human polypeptide. The specification describes novel polypeptides designated PRO201, PRO292, PRO327, PRO346, PRO349, PRO347, PRO357, PRO317, PRO317, PRO509, PRO343, and PRO682. These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumourigenesis. The polypeptides are useful target for the prognosis of tumour treatment. Antibodies against these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New anti-polypeptide antibody useful in the treatment neoplastic cell growth and proliferation -
                                                                                                                                                                                                          MRPLLVLLLIGLAAGS PPLDDNKI PSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGRDGAPG
APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
                                                                                                        APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                                                                                               MRPLLVLLLIGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
                                                                            APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                                                                                                                                                                                                  100.0%;
ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   mammals.
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                                                                                                                                                                                                                                                                                  Score 1325; DB 21; Pred. No. 5.3e-103; ; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide'
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   Best Local Similarity Matches 243; Conserv
                                  Query Match
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16-DEC-1998;
22-DEC-1998;
                                                                                                   polypeptides which are designated as PRO polypeptides are described The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources.
                                                                                                                                                                                                                                                                                                             New human nucleic acids encoding secreted and transmembrane polypeptides, designated as PRO polypeptides, useful as pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243; PRO715; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347; PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide; antibody; screening; detection; inhibition; probe; primer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB01318;
                                                                                                                                                                                                                             New human nucleic acids encoding secreted and transmembrane
                                                                                                                                                                                                                                                              Claim 12; Fig 18; 187pp; English.
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Hillan KJ,
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                                                                      Sequence
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N-PSDB; AAA49560.
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                                                                                                                                                                                                                                                                                              diagnostic agents
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W, Kljavin IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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ME, Goddard
 100.0%; (ilarity 100.0%; )
Conservative 0;
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98US-0112850.
98US-0113296.
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J, Napier MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "N-myristoylation
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1, Godowski
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   Score 1325; DB 21;
Pred. No. 5.3e-103;
); Mismatches 0;
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i PJ, Grimaldi CJ, Gurn
, Roy MA, Tumas D, Woo
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Wood WI;
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Gaps
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RESULT 8
AAU12352
ID AAU1352
ID AAU1352
AC AAU1
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Huma
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Huma
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PR 01-0
PR 01-0
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24-FEB-2000

01-MAR-2000

20-MAR-2000

20-MAR-2000

11-MAR-2000

11-MAY-2000

17-MAY-2000

10-NOV-2000

02-JUN-2000

01-MAY-2000
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01-DEC-1999
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20-DEC-1999
30-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ecretory and transmembrane;
prostate; cervical; tumour
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                                                 2000WO-US07532.
2000WO-US08439.
2000WO-US13705.
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2000WO-US00376.

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2000WO-US04341.

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2000WO-US07377.
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99WO-US30911.
99WO-US30999.
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99US-0170262.
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RESULT 9
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Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   breast, prostate, rectal, cervical of liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or
 Human TANGO
                                28-MAR-2001
                                                              AAB65815;
                                                                                             AAB65815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12172-AAU12446 represent novel human secretory and transmembrane polypeptides. The PRO polypeptides are useful to detect other polypeptides, to link bioactive molecules to cells expressing polypeptides, to modulate biological activities of cells expressing polypeptides, and to detect the presence of mammalian lung, colon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lated, secretory and transmembrane PRO polypeptide used to detect
er PRO polypeptides, link bloactive molecules to cells expressing
phlypeptides, and detect the presence of mammalian tumours e.g.
g, breast, prostate, cervical
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                                                                                             standard;
                                                                                                                                                                            VFA
                                                                                                                                                                                                                                      FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
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Stewart TA,
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Tumas D,
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A, Godowski PJ, Gurney AL, Sh
Numas D, Watanabe CK, Wood WI,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1325; DB 22;
Pred. No. 5.3e-103;
); Mismatches 0;
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L, Sherwood S;
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences human and murine secreted or transmembrane proteins TANGO 253, 7 TANGO 281 and INTERCEPT 258. These are useful in the treatment coronary, pulmonary, olfactory, immunological, neurological, developmental and kidney disorders.
                                         Human adipocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acids for treating diseases and disorders, e.g. atherosclerosis, infection, autoimmune diseases, obesity, ear disorders, brain disorders, tumors, diabetes, arthritis, multiple
                                                                                                13-MAR-2001
                                                                                                                                                     AAB49593;
                                                                                                                                                                                                       AAB49593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
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                                      complement related protein homolog zsig39.
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Pred. No. 5.3e-103;
; Mismatches 0;
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gene

therapy;

complement inhibition; Clq domain;

e.

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to human adipocyte complement related protein homolog, zacrp5 protein and coding sequence (see AAB49590 a) AAC90045). ZACRP5 has a carboxyl-terminal C1q domain. The zacrp5 generates the contract of the contra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel adipocyte complement related protein homolog,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRPLLVLLLLGLAAGSPPLDDNKI PSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGRDGAPG
                                                                                                                                        FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
                                                                                                                                                                                                                                                                                                                                              APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                                                                                                                                                                                                                                                                                                                                                                                       APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSÅFSAKRSESRVPPPSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
VFA
                                                                                                         FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
                                                                                                                                                                                                                         APLPFDRVLVNBQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fig 1; 121pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
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Pred. No. 5.3e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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RESULT 11 AAB49599

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APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ

180 120 120 60 60

APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ

FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP

APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD

APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD

MRPLLVLLLLGLAAGS PPLDDNKI PSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGRPG

MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG

61 61 Matches Query Match Best Local

243;

Conservative

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Mismatches

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Similarity

100.0%; Score 1325; 100.0%; Pred. No. 5

DB 22; 5.3e-103;

243; 0;

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remodelling, for modulating calcium ion concentration, hormone secretion, DNA synthesis or cell growth, inositol phosphate turnover, arrachidonate release, phospholipase C activation, gastric emptying, hum neutrophil activation or ADCC capability and superoxide anion production zacrp6 gene and protein are also useful as antimicrobial applications, preferably against bacteria and virus, for complement inhibition, for treating acute vascular injury, disseminated intravascular coagulation, arteriosclerosis and for wound healing. The present sequence is human adipocyte complement related protein homolog zsig39. This protein was used in a sequence homology comparison with ZACRP6 protein.
                                                                                                                                                                                                                                                                                                                                                       Novel adipocyte complement related protein homolog, ZACRP6, useful as modulators of neurotransmission and for treating disseminated intravascular coagulation, arteriosclerosis and acute vascular injury
Sequence
                                                                                                                                                                               protein homolog, ZACRP6 protein and coding sequence (see AAB49596 and AAC90051). ZACRP6 has a carboxyl-terminal Cig domain. The zacrp6 gene in located on human chromosome 21q. zacrp6 gene and protein are useful for diagnosing and treating inflammations, for determining arterial remodelling, for modulating calcium ion concentration, hormone
                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-061532/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               superoxide anion produ
wound healing; zsig39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; zacrp6; gene therapy; complement inhib adipocyte complement related protein homolog;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on; hormone secretion; inositol phosphate; arachidonate; ase C activation; gastric emptying; neutrophil activatio anion production; antimicrobial; acute vascular injury;
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                                                                                                                                                                                                                                                                          invention
                                                                                                                                                                                                                                                                                                          Fig 1; 119pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000WO-US14024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of the human and murinę secreted or transmembrane proteins TANGO 253, TANGO 25 TANGO 281 and INTERCEPT 258. These are useful in the treatment of coronary, pulmonary, olfactory, immunological, neurological, developmental and kidney disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acids for treating diseases and disorders, e.g. atherosclerosis, infection, autoimmune diseases, obesity, ear disorders, brain disorders, tumors, diabetes, arthritis, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leiby KR;
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                                                                                                                                                                             APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ 180
   FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
                                            FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP 240
                                                                                                                      APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESLASFFQ
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                                                                                                                                                                                                                                                                                                                                                                       MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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l disorder; kidney disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1323; DB 22;
Pred. No. 7.8e-103;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       developmental and kidney disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of human and murine secreted or transmembrane proteins TANGO 253, TANG TANGO 281 and INTERCEPT 258. These are useful in the treatment of coronary, pulmonary, olfactory, immunological, neurological,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
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neurological disorder; pulmonary disorder; immunological disorder;
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                                                                                                                                                                                                                                                                              Sequence
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Search completed: June 20, 2003, 11:23:01 Job time: 63 secs

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US-09-944-806-42
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US-09-944-907-42
US-09-944-907-362
US-10-123-904-362
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Sequence 362,		362	362		362	362,		362,	362,	362,	362,	362,	362,	362,	362,	362,	362,	362,	•	362,	362,	Sequence 362,	•	362,	Sequence 362,
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ALIGNMENTS

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PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 425
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PRIOR APPLICATION NUMBER: 60/069, 425
PRIOR PILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 12, 1997
PRIOR APPLICATION NUMBER: 12, 1997
                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/944,413
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR APPLICATION NUMBER: 60/069,34
PRIOR APPLICATION NUMBER: 60/069,34
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
                            PRIOR APPLICATION NUMBER: 60/069, PRIOR FILING DATE: December 16, 1 PRIOR APPLICATION NUMBER: 60/069,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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FILING
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Tumas, Daniel
Wood, William
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Kljavin, Ivar
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Grimaldi, Christopher
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Goddard, Audrey
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DATE:
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; ORGANISM: Homo US-09-944-413-42
                                                                                      Query Match
Best Local :
                                                                   Matches
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SEQ ID NO 42
                                                                                                                                                                                            LENGTH: 243
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OR APPLICATION NUMBER: 09/254,311
OR FILING DATE: March 3, 1999
OR APPLICATION NUMBER: PCT/US99/1252
OR APPLICATION NUMBER: PCT/US99/21090
FILING DATE: September 15, 1999
TOR FILING DATE: September 15, 1999
                                                                 Local Similarity
mes 243; Conserv
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US00/14042 FILING DATE: May 22, 2000 APPLICATION NUMBER: PCT/US00/20710
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APPLICATION NUMBER: PCT/US00/05841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US00/03565
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APPLICATION NUMBER: PCT/US99/30095
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FILING DATE: No. US20020156004A1ember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020156004A1ember 30, 1999
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APPLICATION NUMBER: PCT/US98/19330
FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
FILING DATE: December 1, 1998
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FILING DATE: July 28,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: December 18, 1997 APPLICATION NUMBER: 60/070,440
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APPLICATION NUMBER: 60/074,092
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NUMBER: 60/113,296
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                                                         Score 1325; DB 9;
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CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR APPLICATION NUMBER: 60/069,334
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PRIOR FILING DATE: December 11, 1997
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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Tumas, Daniel
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Grimaldi, Christopher
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Filvaroff, Ellen
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FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
FILING DATE: June 22, 1999
APPLICATION NUMBER: PCT/US99/21090
FILING DATE: September 15, 1999
FILING DATE: September 15, 1999
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FILING DATE: No. US20020165143A1ember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020165143A1ember 30, 1999
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APPLICATION NUMBER: 09/218,517
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FILING DATE: December 2
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PCT/US01/06520
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PCT/US00/03565
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CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
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PRIOR FILING DATE: December 11, 1999
PRIOR APPLICATION NUMBER: 60/069,271
PRIOR FILING DATE: December 11, 1999
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PRIOR FILING DATE: December 11, 1997
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Wood, William
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NUMBER: PCT/US98/25108
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  Sequence 42, Application US/09944944
Patent No. US20020173463A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
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FILING DATE: February 28 2000
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FILING DATE: No. US20020168715Alember 30,
APPLICATION NUMBER: PCT/US99/28301
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APPLICATION NUMBER: PCT/US99/28409
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APPLICATION NUMBER: PCT/US00/20710
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APPLICATION NUMBER: PCT/US00/14042
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Botstein, David
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NUMBER: PCT/US99/12252
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CURRENT FILING DATE: 2001-09-26
ERIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
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PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                             OR APPLICATION NUMBER: 60/075,9
OR FILING DATE: February 25, 199
OR REPLICATION NUMBER: 60/112,85
OR APPLICATION NUMBER: 60/112,85
OR FILING DATE: December 16
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APPLICATION NUMBER: 60/069335
FILING DATE: December 11, 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: February APPLICATION NUMBER: 60
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                                                                        FILING DATE: June 2 APPLICATION NUMBER:
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                                                      FILING DATE:
           LING DATE: September 15, 1999
PLICATION NUMBER: PCT/US99/28409
LING DATE: No. US20020173463Alember 30, 1999
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Grimaldi, Christopher
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NUMBER: 09/216,021
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NUMBER: PCT/US98/25108
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US-09-944-907-42
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Best Local Similarity
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ORGANISM: Homo Sapien
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APPLICATION NUMBER: PCT/US01/06520
FILING DATE: February 28, 2001
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APPLICATION NUMBER: PCT/US00/20710
FILING DATE: July 28, 2000
APPLICATION NUMBER: PCT/US00/32678
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APPLICATION NUMBER: PCT/US00/14042
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Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
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Kljavin, Ivar
Napier, Mary
Roy, Margaret
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                                              Gurney, Austin
Hillan, Kenneth
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NIMBER: PCT/US00/32678
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Pred. No. 2.3e-89;
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US-09-944-907-42
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Matches
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SEQ ID NO 42
LENGTH: 243
TYPE: PRT
NUMBER OF SEQ ID NOS:
SEQ ID NO 42
LENGTH: 243
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/944,907
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR PILING DATE: 2001-05-25
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                                                                                               TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1 CURRENT APPLICATION NUMBER: US/09/944,929
CURRENT FILING DATE: 2001-08-31
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                                                                PRIOR APPLICATION NUMBER: 09/866,028 PRIOR FILING DATE: 2001-05-25
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Wood, William
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Wood, William
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Grimaldi, Christopher
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Napier, Mary
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Hillan, Kenneth
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Filvaroff, Ellen
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Best Local Similarity
Matches 243; Conserv
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CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
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APPLICATION NUMBER: 60/059117
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APPLICATION NUMBER: 60/059122
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APPLICATION NUMBER: 60/059113
FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/059115
APPLICATION NUMBER: 60/059352
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APPLICATION NUMBER: 60/059588
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Gurney, Austin L.
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Watanabe,Colin K
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APPLICATION NUMBER: 60/063561
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APPLICATION NUMBER: 60/063550
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APPLICATION NUMBER: 60/073612
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APPLICATION NUMBER: 60/063755
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FILING DATE: 1997-10-24
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APPLICATION NUMBER: 60/072320
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FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081229
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APPLICATION NUMBER: 60/081817
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CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
                                                                        Prior Applic
                                                                                                                                                 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME
                              LENGTH: 24
TYPE: PRT
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              ORGANISM: Homo Sapien
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Local Similarity 100.0%;
hes 243; Conservative 0;
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DR FILING DATE: 1998-06-26
DR APPLICATION NUMBER: 60/091360
DR FILING DATE: 1998-07-01
DR APPLICATION NUMBER: 60/091519
DR FILING DATE: 1998-07-02
DR FILING DATE: 1998-07-02
DR PILICATION NUMBER: 60/091982
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Watanabe, Colin K
Wood, William
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Godowski, Paul J.
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Filvaroff, Ellen
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LENGTH: 243
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ORGANISM: Homo
-10-123-904-362
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CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wrap
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                                                                                                               MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
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Watanabe, Colin K
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5. US20030022328A1
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Pred. No. 2.3e-89;
Mismatches 0;
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             US-09-796-753-68
                           RESULT 11
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CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or Fi
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 362
LENGTH: 243
TYPE: PRT
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Best Local
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Filvaroff, Ellen
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Godowski, Paul J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumas, Daniel
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    See Palm or File Wrapper

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US-09-796-753-68
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SEQ ID NO 68
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Publication No.
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CURRENT FILING DATE: 2001-03-01
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                                               Score 1325; DB 9;
Pred. No. 2.3e-89;
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US-10-175-746-362
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US-10-175-746-362
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CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT FILING DATE: 2002-06-19
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NUMBER OF SEQ ID N
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                                                                         APLPFDRVLVNEQGHYDAVIGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ 180
                                                                                                                                       APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD
                    FFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP 240
RFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLVYSDWHSSP
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Wood, William
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Pred. No. 2.3e-89;
); Mismatches 0;
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US-10-176-921-362
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US-10-176-918-362
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CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File WI
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 362
LENGTH: 243
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 243; Conservative 0
                                Sequence 362, Application US/10176921 Publication No. US20030027276A1 GENERAL INFORMATION:
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APPLICANT: Baker, Kevin P. APPLICANT: Beresini, Maur
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Wood, William
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Godowski, Paul J.
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Gerritsen, Mary E.
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Filvaroff, Ellen
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 Beresini, Maureen
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Pred. No. 2.3e-89;
); Mismatches 0;
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GENERAL INFORMATION

APPLICANT:

Baker, Kevin P.

APPLICANT:

APPLICANT:

APPLICANT:

Sherwood, Steven Smith, Victoria

Godowski,Paul J. Gurney,Austin L.

Watanabe, Colin K

Stewart, Timothy A. Tumas, Daniel APPLICANT: APPLICANT: APPLICANT:

APPLICANT:

Gerritsen, Mary E. Goddard, Audrey

Gao, Wei-Qiang

Beresini,Maureen DeForge,Laura Desnoyers,Luc Filvaroff,Ellen Sequence 362, Application US/10137865 Publication No. US20030032155A1

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RESULT 15
US-10-137-865-362
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 362
LENGTH: 243
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Best Local Similarity 100.
Matches 243; Conservative
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CURRENT FILING DATE: 2002-06-20
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C288
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Godowski, Paul J.
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Filvaroff, Bllen
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Pred. No. 2.3e-89;
); Mismatches 0;
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APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C154
CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT APPLICATION NUMBER: US/10/137,865
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 362
LENGTH: 243
TYPE: PRT
ORGANISM: Homo Sapien
US-10-137-865-362

US-10-137-865-362

TABLE TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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                                                                        241 VFA 243
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                                      VFA 243
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Search completed: June 20, 2003, 11:39:57 Job time : 424 secs

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OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Copyright (c) 1993 - 2003 Compugen Ltd.
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
217	218.5	219	219.5	219.5	219.5	219.5	220	220	220	221	221	221.5	222	222.5	222.5
16.4	16.5	16.5	16.6	16.6	16.6	16.6	16.6	16.6	16.6	16.7	16.7	16:7	16.8	16.8	16.8
283	1453	671	1466	673	381	247	380	341	248	1019	886	170	360	1759	1758
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T29980	S21626	CGRT1S	CGHU7L	CGBO6C	T27806	LNRBPS	T28888	T16296 .	LNDGPS	A32856	I50694	B57131	T37285	T29351	T29350
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ALIGNMENTS

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JC4708		OY 145 CQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWPKPASLSGGAMVRLEPEDQ 204	Qy 85 EAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFT 144	Qy 25 PSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGRDGAPGAFGEKGEGGRPGLPGPRGDPGPRG 84	Query Match 91.1%; Score 1207; DB 2; Length 219; Best Local Similarity 100.0%; Pred. No. 1.3e-77; Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	A;Experimental source: adult uterus; clone DKFZp586B0621 C;Genetics: A;Note: DKFZp586B0621.1 C;Superfamily: complement Clq carboxyl-terminal homology	A;Accession: T14782 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-219 <ott> A;Cross-references: EMBL:AL110261</ott>	C;ACCESSION: 114702. R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, August 1999 A:Reference number: Z18184	T14782 hypothetical protein DKFZp586B0621.1 - human (fragment) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Sep-2000 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Sep-2000
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A;Reference number: S30085
A;Accession: S30086
A;Molecule type: DNA
A;Residues: 'TIPFYGWVCULL',52-680 <APT>
A;Cross-references: EMBL:X65120; NID:g23129
A;Note: the initial difference is probably of R;Apte, S; Mattei, M.G.; Olsen, B.R.
FEBS Lett. 282, 393-396, 1991
                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence revision 03-Nov-1995 #text change 22-Jun-1999
C;Accession: S26396; S30086; S15826; S18249; A43901; I51870; S21856
R;Reichenberger, B.; Beier, F.; LuValle, P.; Olsen, B.R.; von der Mark, K.; Bertling,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: adipose tissue R;Nakano, Y.; Tobe, T.; Choi-Miura, N.H.; J. Biochem. 120, 803-812, 1996
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                                                                                                                                                                                 submitted to the EMBL Data Library, A; Reference number: S30085
                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-680 <R
                                                                                                                                                                                                                                                                                                                                                          A; Reference number: S26396; MUID: 93012005;
                                                                                                                                                                                                                                                                                                                                                            A; Title: Genomic organization and full-length cDNA sequence of human A; Reference number: S26396; MUID:93012005; PMID:1397333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N; Alternate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             collagen alpha 1(X) chain precursor - human
                                                                                                                                                                                                                                                        A; Cross-references: EMBL: X68952;
                                                                                                                                                                                                                                                                                                                                  A; Accession: S26396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: protein;Residued: 19-38;93-100;101-112;135-149;173-178 <NAK>;Comment: This protein is an endogenous factor that binds with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title: Isolation and characterization of GBP28, a novel gelatin-binding; Reference number: JC4944; MUID:97103474; PMID:8947845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: unassigned collagens; complement Clq carboxyl-terminal homology; Superfamily: unassigned collagens; complement Clq carboxyl-terminal homology; Keywords: adipose tissue; glycoprotein; hydroxyproline; keywords: adipose tissue; glycoprotein; hydroxyproline; lagrand sequence #status predicted <SIG>
11-18/Domain: signal sequence #status protein #status experimental <MAT>
13-244/Product: gelatin-binding 28kDa protein #status experimental <MAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42-107/Region: collagen-like
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95/Modified site: 4-hydroxyproline (Pro) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114-241/Domain: complement Clq carboxyl-terminal homology <ClQ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNGLYADNDNDSTFTGFLLYHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEGAYVYRSAFSV-GLETYVTIP-NMPIRFTKIFYNQQNHYDGSTGKFHCNIPGLYYFAY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLPGRDGRDGAPGAPGEKGEGGRPGLPGPRGD----
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                                                                                                                                                                                                                                                           EMBL:X72578; EMBL:X72579;
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Pred. No. 7.7e-23;
                                                                                                                                                                                                           March 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235
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A;Note: ----
R;Reichenberger, B.; Alguer, ...
R;Reichenberger, B.; Alguer, ...
Dev. Biol. 148, 562-572, 1991
A;Title: In situ hybridization studies on the expression
A;Title: In situ hybridization studies on the expression
A;Title: A43901; MUID:92077285; PMID:1743401
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A; Residues: 561-647, 'G', 649-666 < AP2>
A; Residues: 561-647, 'G', 649-666 < AP2>
A; Cross-references: EMBL; X58879; NID:g30013; PIDN:CAA41686.l;
A; Thomas, J.T.; Cresswell, C.J.; Rash, B.; Nicolai, H.; Jones,
Blochem. J. 280, 617-623, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 520-597, '7, '599-680 <WAL>
A;Residues: 520-697, '7, '599-680 <WAL>
A;Cross-references: GB:S68531; NID:g545180; PIDN:AAC60615.1; PID:g545181
A;Note: mutant sequence from patient with metaphyseal chondrodysplasia ta;Note: a second mutant sequence with 614-Pro is also described
C;Comment: Prolines and lysines at the third position of the tripeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X60382; NID:g30094; PIDN:CAA42933.1; PID:g30095 A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 if R;Reichenberger, E.; Aigner, T.; von der Mark, K.; Stoss, H.; Bertling,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Cloning of human alpha-1(X) collagen DNA and localization A;Reference number: S15826; MUID:91243838; PMID:2037056
                                                                                                                                                                                                                                                                                                                                                   F;520-680/Domain: amino-terminal nonhelical #status predicted <NCl>F;553-679/Domain: complement Clq carboxyl-terminal homology <ClQ>F;617/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homolog C;Reywords: colled coil; extracellular matrix; glycoprotein; homotrimer; hydroxylysin F;1-18/Domain: signal sequence #status predicted <SIG> F;19-680/Product: collagen alpha 1(X) chain #status predicted <MAT> F;19-56/Domain: amino-terminal nonhelical #status predicted <NC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: I51870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 547-656 <1
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A; Residues: 1-26, 'T', 28-680 < THO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: structural component of extracellular fibrous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: a defect in this gene may cause Schmid metaphyseal chondrodysplasia C;Complex: type X collagen may be a homotrimer
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A;Introns: 52/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Amino acid substitutions of conserved residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                              57-519/Region: interrupted helical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: GDB:128635; OMIM:120110
                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                             Query Match
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461 GFPGSKGDPGSPGPPGPAGIATKGLNGPTGPPGPPGPRGHSGEPGLPGPPGPPGPPGQAV 520
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                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                            GSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLP 74
                                                                                                                    GNPGLPGPKGDPGVGGPPGLPGPVGPAGAKGMPGHNGEAGPRGAPGIPGTRGPIGPPGIP
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                                                                                                                                                                                                                                                                 31.6%;
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Pred. No. 5.
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, T.; Solomon,
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521

MPEGFIKAGORPSLSGTPLVSANQGVTGMPVSAFTVILSKAY--PAIGTPIPFDKILYNR 578

PRSAFSAKRSESRVPPPSDAPLPFDRVLVNE 132

Matches	ļ
Best Loca	
Ouery Mat	Db 586 RIPGLYYFSYHVHAKGTNVWVALYKNGSPVMYTYDEYQKGYLDQASGSAVIDLMENDQ 643
F;19-674/Pr F;547-673/D	GVYYFAVHATVYRASLQFDLVKNGESIA-SFFQFFGGWPKPASLSGGA
F;1-18/Doma	Db 528 GMSFMKAGANQALTGMPVSAFTVILSKAYPGATVPIKFDKILYNRQQHYDPRTGIFTC 585
C;Superfami	Qy 102
C;Genetics:	468 PGPAGIATKGLRGPMGPPGPPGPKGNSGEPGLPGPPGPPGPPGPPGQS
A; Cross-ref	
A; Molecule	מינים ליים ביים ביים מינים
A;Reference	Db 408 AGPPGLPGPVGPOGVKGVPGINGEPGPBGTBGTBGTGDPGMPGALPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAPGAP
A;Title: Is	рстрсинсѕо
R; Thomas, J	
C;Date: 21- C;Accession	cal Similarity 36.0%; Pre
C;Species:	Orone Match
	F;631/Binding site: Garbohydrate (Asn) (Govelent) #status experimental F;611/Binding site: Garbohydrate (Asn) (Govelent) #status experimental
	C;Keywords: Coiled Coil; extracellular matrix; glycoprotein; homotrimer; hydroxyproline; F;1-18/Domain: signal sequence #status predicted <sig></sig>
Db 2	C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology
Q Q	A:Molecule type: protein
Db 1	A;Cross-references: EMBL:M13496; NID:g211699; PIDN:AAA48736.1; PID:g211700 A;Accession: S77711
20/	629, PQAVLSLISWRTIKCGSSCQIQNPMVSIPLNMFILLSQVSYLLKSNNIPLTMS' <nin1></nin1>
당 !	,
07	A;Title: The developmentally regulated type X collagen gene contains a long open reading
שלם	R;Ninomiya, Y.; Gordon, M.; van der Rest, M.; Schmid, T.; Linsenmayer, T.; Olsen, B.R.
γQ	A;Molecule type: mRNA A;Residues: 1-75 <luv></luv>
DЬ	ID:2461368
20	A;Title: The type X collagen gene. Intron sequences split the 5'-untranslated region and
. Matches	R; LuValle, P.; Ninomiya, Y.; Rosenblum, N.D.; Olsen, B.R.
Query Mat Best Loca	A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-674 <nin></nin>
F;122-245/I	
A;Cross-ref C;Superfami	in ExtraceLiular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Pre A;Title: The molecular biology of collagens with short triple-helical domains.
A; Molecule A; Residues:	eorgon,
A;Status: I	ISO218
A;Reference	C;Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text change 13-Aug-1999
	N'Alternate names: type X collagen
K; Petry, F Eur. J. Bio A:Title: I:	S23297 Collagen alpha 1(X) chain precursor - chicken
C; Accession	RESULT 4
C;Species:	Db 637 SGSAIIDLTENDQVWLQLPNAESNGLYSSEYVHSSFSGFLV 677
RESULT 5 S29328	QY 192 SGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLV 232
	Db 579 QQHYDPRTGIFTCQIFGIYYFSYHVHVKGTHVWVGLYKNGTPVMYTYDEYTKGYLDQA 636
oda •	QY 133 QGHYDAVTGKFTCQVPGVYYFAVHATTVYRASLQFDLVKNGESIA-SFFQFFGGWPKPASL 191

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644 VWLQLPNSESNGLYSSEYVHSSFSGFL 670
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Matches 103; Conservative
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Superfamily: complement subcomponent Clq chain A; complement Clq carbo:
122-245/Domain: complement Clq carboxyl-terminal homology <ClQ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary Molecule type: mRNA Residues: 1-246 <PET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uplement subcomponent Clq chain C -
Species: Mus musculus (house mouse)
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ccession: S29328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leference number: S29328; MUID:93011118; PMID:1396691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ccession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolation, sequence analysis and characterization of cDNA clones coding
                                                                                                                                                                   172
                                                                                                                                                                                                              129 TTQY-PEANALVRENSVYTNPQCHYNPSTGKFTCEVPGLYYF-VYYTSHTANLCVHLNLN 186
                                                   232 VYSD 235
                                                                                                       187 LARVASFCDHMFN-SKQVS-SGGALLRLQRGDEVW--LSVNDYNGMVGIEGSNSVFSGFL 242
                                                                                                                                                                                                                                              112 ESRVPPPSDAPLPFDRVLVNBQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKN 171 : | : | : | : | : | . | . | . | . |
243 LFPD 246
                                                                                                                                                                                                                                                                                                                     69 TOGPKGOKGEPGMPGHRGKNGPRGTSGLPGDPGPRGPPGEPGVEGRYKOKHOSVFTVTRO 128
                                                                                                                                                                                                                                                                                                                                                        61 APGEKGEGGRPGLPGPRGDPGPRGEA----GPAGPTGPAGECSVPPR------SAFSAKRS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                  15 LLLLFLLAL----PL-RSQASAGCYGIPGMPGAPGKDGHDGLQGPKGEPGIPAVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 LLVLLLIGLAAGSPPLDDNKIPSLC---PGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                          GESIASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.1%; Score 412; DB 2; Length 246; 42.2%; Pred. No. 5.4e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                  68
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Thomas, J.T.; Kwan, A.P.L.; Grant, M.B.; Boot-Handford, R.P. ochem. J. 273, 141-148, 1991
Ordem. J. 273, 141-148, 1991
Itle: Isolation of cDNAs encoding the complete sequence of bovine type X collage. Reference number: S13301; MUID:91113131; PMID:1703407
Accession: S13301 llagen alpha 1(X) chain precursor - bovine pecies: Bos primigenius taurus (cattle) pecies: 21-Nov-1993 #sequence_revision 23-Feb-1996 #text_change 13-Aug-1999 ccession: S13301

Molecule type: mRNA Residues: 1-674 <THO> ross-references: EMBL:X53556; NID:g263; PIDN:CAA37624.1; PID:g264 ene: COL10A1

Superfamily: collagen alpha i(VIII) chain; complement Clq carboxyl-terminal homol. (Reywords: colled coll; extracellular matrix; glycoprotein; homotrimer l-18/Domain: signal sequence #status predicted <SIG>
19-674/Product: collagen alpha 1(X) chain #status predicted <MAT>
547-673/Domain: complement Clq carboxyl-terminal homology <ClQ>

hery Match lest Local Similarity 96; 31.1%; Score 411.5; DB 2; Pred. No. 1.6e-21; 14; Mismatches 84; Length 674;

Conservative

34;

Indels 61;

Gaps

6

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A,Molecule type: mRNA
A,Residues: 1-12,'F',14-26,'S',28-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,
A,Residues: 1-12,'F',14-26,'S',28-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,
R,R;Apte, S.S.; Seldin, M.F.; Hayashi, M.; Olsen, B.R.
Bur. J. Biochem. 206, 217-224, 1992
Bur. J. Biochem. 206, 217-224, 1992
A,Title: Cloning of the human and mouse type X collagen genes and mapping of the mouse
A, Paference number: 148299; MUID:92267014; PMID:1587271
A;Residues: 52-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L',501-566,'C' A;Cross-references: EMBL:X65121; NID:g50482; PIDN:CAA46237.1; PID:g667031 R;Summers, T.A.; Irwin, M.I.; Mayne, R.; Balian, G. J. Biol. Chem. 263, 581-587, 1988 J. Biol. Chem. 263, 581-587, 1988 A;Title: Monoclonal antibodies to type X collagen. Biosynthetic studies using an all A;Title: Monoclonal antibodies to type X collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X67348; NID:g50480; PIDN:CAA47763.1; PID:g50481 R;Elima, K.; Metsaeranta, M.; Kallio, J.; Peraelae, M.; Eerola, I.; Garo Biochim. Biophys. Acta 1130, 78-80, 1992 A;Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1 A;Reference number: S22215; MUID:92182017; PMID:1543751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:Z21610; NID:g49793; PIDN:CAA79736.1; P. R;Blina, K.; Eerola, I.; Rosati, R.; Metsaeranta, M.; Garofalo, Biochem. J. 289, 247-253, 1993
A;Title: The mouse collagen X gene: complete nucleotide sequence A;Reference number: $28807; MUID:93143676; PMID:8424763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
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A;Residues: 385-450,'K',452-627 <ELA>
A;Cross-references: EMBL:X63013; NID:g49795; PIDN:CAA44741.1;
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A;Residues: 1-285,'A',287-680 <ELI>
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                                                                                                                                                                                                                        A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
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J. Biochem. 213, 99-111, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;553-679/Domain: complement Clq carboxyl-terminal homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Introns: 51/3
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  TYDEYSKGYLDQA--SGSAIMELTENDOVWLQLPNAESNGLYSSEYVHSSFSGFLV
                                  SFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFLV 232
                                                                                                            PSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNG-ESIA
                                                                                                                                                      LPGPPGPPGPPGQAVMPDGFIKAGQRPRLSGMPLVSANHGVTGMPVSAFTVILSKAY--P
                                                                                                                                                                                            --GPAGPTGPAGECSVP-----
                                                                                                                                                                                                                                                                      GLPGRDGRDGAPGAPGEKGEGGRPGLPGPR----
                                                                                                                                                                                                                                                                                                            GEPGLNGPK-----GNPGLPGQKGDPGVGGTPGLRGPVGPVGAKGVPGHNGEAGPRGEP
                                                                                                                                                                                                                                                                                                                                                GSPPLDDNKI PSLCPGHPGLP---
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        30.8%; Score 408; DB 2; 33.4%; Pred. No. 2.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                    34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PMID:2826450
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                                                                                                                                                                                            PRSAFSAKRSESRVPP
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                                                                                                                                                                                                                                                                                                                                                                                        88;
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
  677
                                                                                                                  176
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                                                                              623
                                                                                                                                                      563
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RESULT C1HUQC

complement subcomponent Clq chain C N;Alternate names: complement subcom C;Species: Homo sapiens (man) subcomponent Clq gamma chain

C; Accession: S14351; A03207 ;Date: 22-May-1981 #sequence_revision 31-May-1996 #text_change 22-May-1998

R;Sellar, G.C.; Blake, J. 274, 481-490, 1991 D.J.; Reid, K. B.M

A; Title: A; Status: not compared with A;Accession: S14351 A;Reference number: S14350; Characterization and organization nce number: S14350; MUID:91174759; conceptual translation of the genes encoding PMID:1706597 the Α-,

C-Ch

A;Residues: A;Molecule type: -245 <SEL> DNA

Reid, K.B.M.

Biochem. J. 179, 367-371, 1979
A;Title: Complete amino acid sequences of the three collagen-like
A;Reference number: A90304; MUID:80020137; PMID:486087 regions

A; Accession: A03207

A;Residues: 29-56,'P',58-65,'K',67-71,'P',73-83,'K',85-86,'D',88-89,'N',91-122 <REI>C;Comment: The first component of complement is a calcium-dependent complex of the trivation of C1r (enzyme), C1s (proenzyme), and the other eight components of compleme C;Comment: The C1q subcomponent is composed of nine subunits, six of which are disuldimers of the C chain. Equimolar amounts of the A, B, and C chains are found after A;Gene: GDB:C1QG C;Genetics A; Molecule type: protein

A;Cross-references: GDB:128132; OMIM:120575
A;Map position: 1p36.3-1p34.1
A;Introns: 60/3
A;Introns: 60/3
C;Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal C;Superfamily: complement pathway; glycoprotein; homodimer; hydroxylysine; hydroxyproli F;1-28/Domain: signal sequence #status predicted <SIG>

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A;Cross-references: GB:J05042; NID:g164895; PIDN:AAA31204.1; PID: C;Superfamily: collagen alpha 1(VIII) chain; complement Ciq carbo F;1-20/Domain: signal sequence #status predicted <SIG-F;21-744/Product: collagen alpha 1(VIII) chain #status predicted F;21-744/Product: collagen alpha 1(VIII) chain #status predicted F;21-117/Region: amino-terminal nonhelical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collagen alpha 1(VIII) chain precursor - rabbit C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
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A34246
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F;31-124/Domain: complement C1q carboxy1-terminal homology <C10>
F;121-244/Domain: complement C1q carboxy1-terminal homology <C10>
F;32/Disulfide bonds: interchain #status experimental
F;36,39,42,45,54,63,81,93,96,99,105/Modified site: 4-hydroxyproline (Pro)
F;36,39,42,45,54,63,81,93,96,99,105/Modified site: 4-bydroxyproline (Pro)
F;57,72,75/Modified site: 5-hydroxylysine (Lys) #status experimental
F;75/Binding site: carbohydrate (Lys) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 264, 16022-16029, 1989
A;Title: The cloning and sequencing of alphal (VIII) omains similar to those of type X collagen.
A;Reference number: A34246; MUID:89380199; PMID:2470
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F;572-744/Region:
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A; Residues: 1-744 < YAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: A34246;
A;Accession: A34246
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R; Yamaguchi, N.; Ber
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                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKNGESIASFFQFFGGWPKPASL-SGGAMVRLEPEDQVWVQVGVGDY---IGIYASIKTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APGAPGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPP-----RSAFSA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKLLLLLLLLALR------GQANTGCYGIPGMPGLPGAPGKDGYDGLPGPKGEPGIPA
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                                                                                                                                 PGVAGLHGPPGKPGALGPQGQPGLPGPPGPPGPPGPPAVMPPTPAPQGEYLPDMGLGIDG 594
                                                                                                                                                                                                                                                                    IPSLC--PGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I PGIRGPKGQKGEPGLPGHPGKNGPMGPPGMPGVPGPMGIPGEPGEEGRYKQKFQSVFTV
CQVPGVYYFAVHATVYRASLQFDLVKNGESIA-SFFQFFGGWPKPASLSGGAMVRLEPED
                                          VKTPHAYAAKKGKNGGPAYEMPAFTAELTAPFPPVGAPIKFDRLLYNGRQNYNPQTGIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Benya, P.D.; van
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                                                                                                                                                                                                                                                                                                                                                                                                                             interrupted helical carboxyl-terminal nonhelical
                                                                                                                                                                                                                                                                                                                                                                                                     complement Clq carboxyl-terminal homology
                                                                                         -AFSAKRSESRVP---
                                                                                                                                                                             -GPRGDP---GPRGE---AGPAGPTGPAGECSVPPRS-----
                                                                                                                                                                                                                                                                                                                                    28.2%;
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                                                                                                                                                                                                                                                                                                                                    Score 374;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              der Rest, M.; Ninomiya,
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                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                    .6e-19;
                                                                                    PPSDAPLPFDRVLVNEQGHYDAVIGKFT
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R;Muragaki, Y.; Shiota, C.; Inoue, M.; Ooshima, A.; Olsen, Bur. J. Biochem. 207, 895-902, 1992
A;Title: Alpha-1(VIII)-collagen gene transcripts encode a A;Reference number: \$23779; MUID:92362626; PMID:1499564

#text_change

16-Jun-2000

short-chain collagen B.R.; Ninomiya, Y.

poly

C; Accession: S23779

A;Cross-references: EMBL:X66976; NID:g50493; PIDN:CAA47387.1; PID:g1359953 C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-termi F;616-742/Domain: complement Clq carboxyl-terminal homology <ClQ>

A; Molecule type: DNA A; Residues: 1-743 < MUR>

Query Match

Local Similarity

32.8%;

27.4%; Score 363.5; DB 1;

Length 743;

Clq carboxyl-terminal homology <C1Q>

Pred. No.

4.1e-18;

Mismatches

Indels

71;

Gaps

Matches

A;Status: preliminary

A; Reference number: S23779; A; Accession: S23779

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collagen alpha 1(VIII) chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collagen alpha 1(VIII) chain - chicken
c;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S23298
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A; Residues: 1-744 <NIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  VPGLLGPKGEPGIPGDQGLQGPPGIPGITGPSGPIGPPGIPGPKGEPGLPGPPGFPGVGK 534
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                                                                                                                                                                                                                                                                                               VKTPHAYAAKKGKNGGPAYEMPAFTAELTAPFPPVGAPIKFDRLLYNGRQNYNPQTGIFT
                                                                                                                                                                                                                                                                                                                               ----AFSAKRSESRVP------PPSDAPLPFDRVLVNEQGHYDAVTGKFT
                                                                                                                                                                                                                                                                                                                                                                          PGVAGLHGPPGKPGALGPQGQPGLPGPPGPPGPPGPPAVMPPTPAPQGEYLPDMGLGIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPSLC--PGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLP-----
                                                                                                                                                                                                                                                         CQVPGVYYFAVHATVYRASLQFDLVKNGESIA-SFFQFFGGWPKPASLSGGAMVRLEPED
                                                                                                                                                                                                                                                                                                                                                                                                            ----GPRGDP---GPRGE---AGPAGPTGPAGECSVPPRS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sandell L.J. and Boyd C.D., eds., pp.79-114, of collagens with short triple-helical domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 370; DB 1;
Pred. No. 1.4e-18;
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C;Species: Homo sapiens (man)
C;Date: 03-Nov-1995 #sequence_revision
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 266; 7721-7727, 1991 ... Practet, M.O.; NIDOMIYA, A; Title: The alpha2(VIII) collagen gene. A novel member of the A; Reference number: A57131; MUID:91210292; PMID:2019595 A; Accession: A57131
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A; Residues: 1-635 < MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Muragaki, Y.; Jacenko, O.; Apte, S.; Mattei, M.G.; Ninomiya, Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
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RESULT
C1HUQB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: collagen alpha 1(VIII) chain; complement Clg carboxyl-terminal;1-11/Domain: amino-terminal nonhelical (fragment) #status predicted <NC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;12-468/Region: interrupted helical ;12-468/Region: interrupted helical #status predicted;469-635/Domain: carboxyl-terminal nonhelical #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GB:M60832; NID:g177178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: A57131
                     13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIDGVKTPHAYAGKKGKHGGPAYEMPAFTAELTVPFPPVGAPVKFDKLLYNGRQNYNPQT
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                                                                                                                                                                                VPATYTYDEYKKGYLDQA-
                                                                                                                                                                                                                         -ESIASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFL
                                                                                                                                                                                                                                                                        PL--PASGMPVKFDRTLYNGHSGYNPATGIFTCPVGGVYYFAYHVHVKGTNVWVALYKNN
                                                                                                                                                                                                                                                                                                   SRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNG 172
                                                                                                                                                                                                                                                                                                                                                              PĠĹPĠPPĠAPĠAPDÉTĠIĀĠLHLPNĠGVEGAVLGKGGKPQFGLĠĖLŚAHATPĀFTĀVLTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
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Pred. No. 3
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                                                                                                                                                                                  SGGAVLQLRPNDQVWVQIPSDQANGLYSTEYIHSSFSGFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN: AAA62822.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.8e-18;
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C;Date: 22-May-1981 #sequence_revision 31-May-1996 #text_change
C;Accession: B23422; A23422; B90304; A90301; B90315; A03206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 28-253 <RE1>
A;Cross-references: EMBL:X03084
A;Note: the authors translated R;Reid, K.B.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. J. 179, 367-371, 1979
A;Title: Complete amino acid sequences of the three collagen-like A;Reference number: A90304; MUID:80020137; PMID:486087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 'HS', 1-32 <REI>
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                                                                                                                                                                                                                                                                                                                                           C;Keywords: complement pathway; glycoprotein; heterodimer; hydroxylysine; hydroxypro.
C;Keywords: complement pathway; glycoprotein; heterodimer; hydroxylysine; hydroxypro.
F;12-27/Domain: signal sequence #status predicted <SIG-
F;28-253/Product: complement subcomponent Clq chain B #status experimental <MAT-
F;33-116/Domain: collagenous, triple helix <COL-
F;123-249/Domain: collagenous, triple helix <COL-
F;123-249/Domain: collagenous, triple helix <COL-
F;28/Modified site: pyrrolidone carboxyl-terminal homology <ClQ-
F;31/Disulfide bonds: interchain (to chain A-26) #status experimental
F;35,38,41,53,56,65,83,86,101,104,107/Modified site: 4-hydroxyproline (pro) #status experimental
F;35,38,41,53,56,65,83,86,101,104,107/Modified site: 4-hydroxyproline (pro) #status experimental
F;39,62,77,92,98,110/Modified site: 5-hydroxylysine (Lys) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 28-99,'P',101-195 <RE3>
R;Reid, K.B.M.; Gagnon, J.; Frampton, J.
Biochem. J. 203, 559-569, 1982
A;Title: Completion of the amino acid sequences of the A;Reference number: A90315; MUID:82283890; PMID:6981411
A;Accession: B90315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: A90301; MUID:79041552; A;Accession: A90301
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Biochem. J. 173, 863-868, 1978
A;Title: Amino acid sequence of the N-terminal 108 amino
A;Title: Amino acid sequence of the N-terminal 108 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Reid, K.B.M.; Thompson, B.O.1
Biochem. J. 173, 863-868, 1978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 'E', 29-84,'D', 86-99,'P', 101-135
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A;Residues: 136-253 <RE4>
A;Note: 176-Glx may also be present
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Matches
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                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                            Local
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                                                      73
                                                                                                 64
                                                                                                                                               13
                                                                                                                                                                                                                                                               Similarity
                                                      EPGEKGDPGIPGNPGKVGPKGPMGPKGGPGAPGPKGESGDYKATQKIAFSATRT-IN
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                                                                                                                                                                                                                                                            27.3%; Score 362; DB 1; 36.9%; Pred. No. 1.7e-18;
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complement subcomponent Clq chain B precursor [validated] N;Alternate names: complement subcomponent Clq beta chain C;Species: Homo sapiens (man) human 08-Dec-2000

A;Title: Molecular cloning and characterization of the complementary A;Reference number: A23422; MUID:86076906; PMID:3000358 A;Accession: B23422

DNA and

gene

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second position as Arg; they

residue 46 as

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regions

acid residues 0f the w

Þ and B chains 얁 subcomponent

C;Comment: The first component of complement is a calcium-dependent complex of the the ivation of C1r (enzyme), C1s (proenzyme), and the other eight components of complement C;Comment: The C1q subcomponent is composed of nine subunits, six of which are disult (see PIR:C1HUQC) chain. Equimolar amounts of the A, B, and C chains are found after:

A; Map position: 1936.3-1934.1 C; Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal

LLVILLIJGIAAGSPPLDDNKIPSICPGHPGLPGTPGHHGSQGLPGRDGRDGRDGRDGAPGAPG EKGEGGRPGLPGPRGDPGPRGEAGP------AGPTGPAGECSVPPRSAFSAKRSESR 114 LMLLLLLGLIDISQAQLSCTGPPAIPGIPGIPGTPGPDGQPGTPGIKGEKGLPGLAGDHG Mismatches 100; Length Indels 18; 63 131 72

6

δ 115 VPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGE-

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collagen alpha 1(VIII) chain precursor - human C;Species: Homo sapiens (man) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999 C;Accession: S15435 R;Muragaki, Y.; Mattei, M.G.; Yamaguchi, N.; Olsen, B.R.; Ninomiya, Y. Bur. J. Biochem. 197, 615-622, 1991 A;Title: The complete primary structure of the human alpha-1(VIII) chain and assignment A;Accession: S15435; MUID:91231001; PMID:2029894 A;Accession: S15435
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S15435
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A;Residues: 1-253 <SCH>
A;Cross-references: EMBL:X71127; NID:g510191; PIDN:CAA50440.1; PID:g510192
A;Cross-references: EMBL:X71127; NID:g510191; PIDN:CAA50440.1; PID:g510192
C;Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal homology <C1Q>
F;121-249/Domain: complement C1q carboxyl-terminal homology <C1Q>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             x;Scnwaeble, W.; Petry, F.; Loos, M.
submitted to the EMBL Data Library, March 1993
A;Description: cDNA cloning and expression of the mRNA encoding
A;Reference number: S49158
A;Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement protein C1q beta chain precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 16-Feb-1995 #sequence_revision 12-May-1995 C;Accession: S49158 R;Schwaeble, W.; Petry, F.; Loos, M. submitted to the EMBL Data Library, March 1993 submitted to the EMBL Data Library, March 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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S49158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                   A; Cross-references:
                                                                                      A; Molecule type: mRNA
A; Residues: 1-744 < MUR>
                                                                                                                                      A;Status: preliminary
Gene: GDB:COLBA1; GDB:128104; OMIM:120251; Gross-references: GDB:128104; OMIM:120251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 VYSD 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRPLLVLLLLGLAAGSPPLDDNKIPSLC---PGHPGLPGTPGHHGSQGLPGRDGRDGRDG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYIGIYASIKTDSTFSGFLVYSD 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APGAP-----GEKGEGGRPGLP---GPRGDPGPRGEAGPAGPTGP---AGECSVPPRSA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLLGVEGA---NSIFTGFLLFPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNI VRGRDRDRMQKVLTFCDYAQNTFQV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FDLVKNG-----ESIASF-----FQFFGGWPKPASLSGGAMVRLEPEDQVWVQ-VGVG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQ 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPGLAGDHGELGEKGDAGIPGIPGKVGPKGPVGPKGAPGPPGPRGPKGGSGDYKATQKVA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTPLL-LLLLGL-----LHVSWAQSSCTGSPGIPGVPGIPGVPGSDGKPGTPGIKGEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFPD 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                     EMBL: X57527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 360.5; DB 2
Pred. No. 2.2e-18;
                                                                     NID:g30081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250
                                                                     PIDN:CAA40748.1; PID:g30082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGGVVLKLEQEEVVHLQATDKN 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
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A;Map position: 3q11.1-3q13.2 (7;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homolc F;1-20/Domain: signal sequence #status predicted <SIG>F;21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>F;21-174/Pegion: amino-terminal nonhelical
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                          S
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                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                    595
                                                                  655
                                                                                                  145
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                                                                                                                                                                                                       535 PGVAGLHGPPGKPGALGPQGQPGLPGPPGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDG 594
                                                                                                                                                                                                                                                                            475
713
                              204 QVWVQVGVGDYIGIYASIKTDSTFSGFLVY
                                                                                                                                                                                                                                          75
                                                                                                                                                                                                                                                                                                             24 IPSIC---PGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLP-----
                                                                                                                                                                                                                                                                                                                                                 , 68
                                                                                                                                                                                                                                                                                                                                                                 Similarity
RVFLOMPSEQAAGLYAGQYVHSSFSGYLLY
                                                                                                COVPGVYYFAVHATVYRASLOFDLVKNGESIA-SFFQFFGGWPKPASLSGGAMVRLEPED 203
                                                                                                                                    VKPPHATGAKKGKNGGPAYEMPAFTAELTAPFPPVGGPVKFNKLLYNGRQNYNPQTGIFT
                                                                                                                                                                        VPPRSAFSAKRSESRVP-----
                                                                                                                                                                                                                                                                            VPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGIPGPKGEPGLPGPPGFPGIGK 534
                                                                  CEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYDEYKKGFLDQA--SGSAVLLLRPGD
                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                         27.1%; Scu
33.0%; Pre
==tive 33;
                                                                                                                                                                                                                                         GPRGDPGPRGEAGPAGPTGP----
                                                                                                                                                                                                                                                                                                                                               Score 359; DB
Pred. No. 8.5e
33; Mismatches
                                                                                                                                                                        -----PPSDAPLPFDRVLVNEQGHYDAVTGKFT 144
742
                                233
                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                 .5e-18;
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                                                                                                                                                                                                                                                                                                                                                                               Length 744;
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                                                                                                                                                                                                                                                                                                                                                 62;
                                                                                                                                                                                                                                            -AGECS
                                                                                                                                                                                                                                                                                                                                               Gaps
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Search completed: June 20, 2003, 11:26:01 Job time : 46 secs

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RESULT 1
CQTS_HMAN
ID _CQTS_H
AC Q9BXJO
DT 15-JUN
DT SEQUEN
RA Sheppa
RA Sheppa
RA Sheppa
RA Wieman
RL Submit
CC -i-SI
CC This S
CC betwee
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CC use betwee
CC moditii
CC entiti
CC ----
DR EMBL;
DR EMBL;
DR TINTS
DR Ffam;
DR Ffam;
DR Ffam;
DR FFAN;
DR FFAN;
DR FFAN;
DR FFAN;
DR SMART;
Query Match
Best Local Similarity
Matches 243; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OMPACATION OR CIKE...
HOMO Sapiens (Human).
Homo sapiens (Human).
Horvota; Metazoa; Chordata; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9BXJO; Q9UFX4;
15-JUN-2002 (Rel. 41, Careated)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Complement-clq tumor necrosis factor-related protein 5 precursor.
ClQTNP5 OR CTRP5.
                                                                                                                                                     SIGNAL
                                                                                                                                                                                       PRINTS; PR00007; COMPLE
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q;
Collagen; Signal.
                                                                                                                                                                                                                                                                                                                                               EMBL; AF329841; AAK17965.1; -. EMBL; AL110261; CAB53702.1; -. Genew; HGNC:14344; ClQTNF5.
                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
-!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Sheppard P.O., Humes J.M.;
"Homo sapiens complement-clq tumor necrosis factor-related protein.";
                                                                                                                                                                                                                                                                     Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ottenwaelder B., Obermaier B., Mewes H.-W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 25-243 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-2000) to the
                                                                                                                                                                                                                                                                                                         InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wiemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Uterus;
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                                                                                                 30
97
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                                                                           AA;
                                                                                                                                                                                                                                                     COMPLEMNTC1Q.
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170
1019
1262
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671
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25298
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243
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100.0%; s
100.0%; F
tive 0;
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CA28 MOUSE
CA16 CHICK
CA13 CHICK
CA13 CHICK
SEPA CANFA
CCDC CABEL
ESPA RABIT
CA13 HUMAN
CA11 MOUSE
CA11 HUMAN
CA12 BOVIN
                                                                                                               POTENTIAL.

COMPLEMENT-C1Q TUMOR PRELATED PROTEIN 5.

COLLAGEN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ
                                                           C1Q.
; 7CCDA65CDA7EB784 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                     Score 1325;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
   ; DB 1;
1.7e-85;
es 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gassenhuber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         databases.
                                                                                                                                                         NECROSIS FACTOR-
                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P06908
P35799
P12842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       he EMBL outstation restrictions on it
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                                       243;
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mus musculu
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canis famil
canorhabdi
coryctolagus
homo saplen
rattus nory
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homo sapien
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Result No.

Match

Length DB

ij

Description

Query

412 411.5 410.5

408 403 397 374

P14282

homo sapien oryctolagus lepomis mac

homo sapien

P02747 Q9bxj5 Q9bxj

homo sapien
mus musculu
homo sapien
homo sapien

424 418.5 417

CQT5 HUMAN
APM1 MOUSE
APM1 HUMAN
CA1A HUMAN
CA1A CHICK
C1QC MOUSE

Q60994 Q15848

Q9bxj0

homo

Bru

musculu sapien

homo sapien

Q03692

P08125

homo sapien gallus gall

mus musculu

bos taurus

373
366.5
366.5
362
360.5
360.5
350
350
314
314
298.5
285.5
280.5
287.5
277.5
277.5
279.5
229.5

CAIA_BOVIN
CQT7 HUMAN
CQT7 HUMAN
CAIA MOUSE
CQT2 HUMAN
CAIA HUMAN
CAIA HUMAN
CAIA HUMAN
CAIA HUMAN
CAIA HUMAN
CIQB MOUSE
CIRF HUMAN
CAIJ HUMAN
CAIJ HUMAN
CAIJ RAT
CAIJ MOUSE

Q9bxj1 Q14050 P13941

rattus homo sapien

Conservative

Mismatches

Indels

0

Gaps

0

Q9bxj4

homo sapien tamias sibi tamias sibi tamias sibi homo sapien mus musculu homo sapien

P04258

tamias sibi bos taurus homo sapien

088992

P98086

mus musculu
homo sapien
mus musculu

Minimum Maximum

DB DB

seq

length: 0 length: 2000000000

Total number of

hits satisfying chosen parameters:

Scoring table: Sequence: Perfect score:

Gapop BLOSUM62

10.0

Gapext 0.5

112892 segs,

41476328 residues

US-09-944-403-42

1 MRPLLVLLLLGLAAGSPPLD.......DSTFSGFLVYSDWHSSPVFA 243

Run on:

June 20,

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summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RESULT APPLIATE APPLI
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Q60994; Q62400;
Q1-NOV-1997 (Rel
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Adiponectin precursor (30 kDa adipocyte complement-related (ACRP30) (Adipocyte specific protein AdipoQ).
APM1 OR ACRP30 OR ADIPOQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishi Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Pukuda Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saitt Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H. Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackeni Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackeni Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Wasakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96209999; PubMed=8631877;
Hu E., Liang P., Spiegelman B.M.;
"AdipoQ is a novel adipose-specif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. TISSUE-Fibroblast;
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MEDLINE-96070757; PubMed-7592907;

MEDLINE-96070757; PubMed-7592907;

Scherer P.E., Williams S., Pogliano
"A novel serum protein similar to Cl
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Das K., Lin Y., Widen
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STRAIN=C57BL/6J; T
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Rodentia;
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Sciurognathi; Muridae;
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Kasukawa T., Saito
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Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts F., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilm Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      runctional annotation of a Nature 409:685-690(2001).
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[6]
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Mori Y., Ide T., Murakami K., Tsuboyama-Kasaoka N., Ezaki O.,
Akanuma Y., Gavrilova O., Vinson C., Reitman M.L., Kagechika
Shudo K., Yoda M., Nakano Y., Tobe K., Nagai R., Kimura S., T
                       use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
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Berg A.H., Combs T.P., Du X., Brownlee
"The adipocyte-secreted protein Acrp30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21372498; PubMed=11479627;
or send an email to license@isb-sib.ch).
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:- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
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                                                                                                     European Bioinformatics Institute.
                                                                                                     SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no rest
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EMBL; U49915; AAB06706.1; --EMBL; AF304466; AAK13417.1; --EMBL; AK003138; BAB22597.1; --MGD; MGI:106675; Acrp30.
InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 1. DOMAIN
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COLLAGEN-LIKE.
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INTERCHAIN (BY SIMILARITY).
HYDROXYLATION (BY SIMILARITY).
HYDROXYLATION (BY SIMILARITY).
HYDROXYLATION (BY SIMILARITY). Repeat; Hydroxylation; Plasma;

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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Adiponectin precursor (30 kDa adipocyte complement-related (ACRP30) (Adipose most abundant gene transcript 1) (apM-1)
                                                                                                                                                                                                                                                                                                            TISSUE=Adipose tissue;
MEDLINE=96224171; PubM
Maeda K., Okubo K., Sh
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hinding protein).
APM1 OR ACRP30 OR GBP28.
                                                                                              MEDLINE=99196984; PubMed=10095105; Saito K., Tobe T., Minoshima S., Asakawa S., Sumiya J., Yoda Nakano Y., Shimizu N., Tomita M.; "Organization of the gene for gelatin-binding protein (GBP28) Gene 229:67-73(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q15848;
                                                                                                                                                                                                                                     "CDNA cloning and expression of a novel adipose specific collagen-like factor, apM1 (AdiPose Most abundant Gene transcript 1).";
Biochem. Biophys. Res. Commun. 221:286-289(1996).
                                                                                                                                                                                                                                                                                            Matsubara K.;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                        Schaeffler A., Orso
                                      MEDLINE=99333693;
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  333693; PubMed=10403784; A., Orso E., Palitzsch Schoelmerich J., Schmit
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Schmitz G.;
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RP VARIANTS ARG-84; MET-117; THR-164; SER-221 AND PRO-241.

RRP VARIANTS ARG-84; MET-117; THR-164; SER-221 AND PRO-241.

RR HATA K., Boutin P., Mori Y., Tobe K., Dina C., Yasuda K., Yamauchi T.,

RA HATA K., Boutin P., Mori Y., Tobe K., Dina C., Yasuda K., Yamauchi T.,

RA Otabe S., Okada T., Eto K., Kadowaki H., Hagura R., Akanuma Y.,

RA Kimura S., Tomita M., Kimura S., Ito C., Froguel P., Kadowaki T.;

RA Kimura S., Tomita M., Kimura S., Ito C., Froguel P., Kadowaki T.;

RR Kimura S., Tomita M., Kimura S., Ito C., Froguel P., Kadowaki T.;

RR Kimura S., Tomita M., Kimura S., Ito C., Froguel P., Kadowaki T.;

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RR Kimura S., Tomita M., Kimura S., Ito Regulation R., Kimura S., Ito C., Froguel P., Kadowaki T.;

RR Kimura S., Tomita M., Kimura S., Ito C., Froguel P., Kadowaki T.;

RR Kimura S., Natano K., Kimura R., Kimura S., Ito C., Froguel P., 
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Akanuma Y., Gavrilova O., Vins
Shudo K., Yoda M., Nakano Y.,
Kadowaki T.,
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MEDLINE=21372498; PubMed=11479627;

MEDLINE=21372498; PubMed=11479627;

Yamauchi T., Kamon J., Waki H., Terauchi Y., Kubota N., Hara K.,

Mori Y., Ide T., Murakami K., Tsuboyama-Kasaoka N., Ezaki O.,

Mori Y., Ide T., Murakami K., Tsuboyama-Kasaoka N., Ezaki O.,

Mori Y., Ide T., Murakami K., Tsuboyama-Kasaoka N., Kagechika H.

Akanuma Y., Gavrilova O., Vinson C., Reitman M.L., Kagechika H.

Akanuma Y., Gavrilova O., Tobe K., Nagai R., Kimura S., Tom
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Ouchi N., Kihara S., Arita Y., Okamoto Y., Maeda K., Kuriyan Hotta K., Nishida M., Takahashi M., Muraguchi M., Ohmoto Y., Hakamura T., Yamashita S., Funahashi T., Matsuzawa Y.;
"Adiponectin, an adipocyte-derived plasma protein, inhibits endothelial NF-kappaB signaling through a cAMP-dependent pat Circulation 102:1296-1301(2000).
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Yokota T., Oritani K., Takahashi I.
Ouchi N., Kihara S., Funahashi T.,
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Horie M., Shimomura I., Hotta K., Kuriyama H.,
Yamashita S., Funahashi T., Matsuzawa Y.;
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                                               PHARMACEUTICAL: Adiponectin might be used diabetes type 2 and insulin resistance. SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN. SIMILARITY: CONTAINS 1 CIQ DOMAIN.
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piated with both lipoatrophy and obesity.";
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Tenner A.J.,
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Kihara S.,
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Pfam; PF01391; Collagen; 1.
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AJ131461; CAB52413.1; JOINED.
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MEDLINE=92267014; PubMed=1587271;

Apte S.S., Seldin M.F., Hayashi M., Olsen B.R.;

"Cloning of the human and mouse type X collagen
the mouse type X collagen gene to chromosome 10.

Bur. J. Biochem. 206:217-224(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Last annotation Collagen alpha 1(X) chain precursor.
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Bertling W.M.;
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Solomon E., Grant M.E., Boot
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MEDLINE=92109659; PubMed=1764025;
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                                                                                                                      MEDIINE=97255959; PubMed=9101290; Kuivaniemi H., Tromp G., Prockop D.J.; Kuivaniemi H., Tromp G., Prockop D.J.; "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-associated collagen (type IX), and network-forming collagen (type X) cause a spectrum of diseases of bone, cartilage, and blood vessels.";
                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 547-655 FROM N.A. MEDLINE=92077285; PubMed=1743401; Reichenberger E., Aigner T., von
                                                                                                                                                                                                                                                                                                                                                                                                             Apre S., Mattei M.-G., Olsen B.R.; "Cloning of human alpha 1(X) collagen COL10A1 gene to the q21-q22 region of FEBS Lett. 282:393-396(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 561-666 FROM N.A. MEDLINE=91243838; PubMed=2037056;
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MEDLINE=94136476; PubMed=8304336; Wallis G.A., Rash B., Sweetman W. Grant M.E., Boot-Handford R.P.;
                                                                                                                                                                                                                             REVIEW ON VARIANTS
                                                                                                                                                                                                                                                                   "In situ hybridization studies
in fetal human cartilage.";
Dev. Biol. 148:562-572(1991).
                                                                VARIANTS
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to the EMBL/GenBank/DDBJ
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                         Sweetman W.A.,
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Boot-Handford
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Catarrhini; Hominidae;
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Bonaventure J., Chaminade F., Marc "Mutations in three subdomains of collagen type X account for most o
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"Type X collagen multimer assembly in
to Val mutation in the alpha 1(X) NC1
metaphyseal chondrodysplasia.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mutations within the gene encoding the alpha 1 (X) chain of type collagen (COL10A1) cause metaphyseal chondrodysplasia type Schmid not several other forms of metaphyseal chondrodysplasia.";

J. Med. Genet. 33:450-457(1996).
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                                                                                                                                                                                                                                                                                                                      "Novel missense mutation resulting in the substitution cysteine at codon 597 of the type X collagen gene assoc Schmid metaphyseal chondrodysplasia.";
J. Hum. Genet. 43:259-261(1998)
-1- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHRO CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Mutation of the type X collagen gene 'COL10A1' spondylometaphyseal dysplasia."; Am. J. Hum. Genet. 63:1659-1662(1998).
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MEDLINE=99057503; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ikegawa S., Nakamura K., Nagano A., Haga N., Nakamura Y.;
"Mutations in the N-terminal globular domain of the type X collagen
gene (COL10A1) in patients with schmid metaphyseal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96375754; PubMed=8782043; Wallis G.A., Rash B., Sykes B., B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT SMCD
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                                                                                                                                                                                                                                                             -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99069781; PubMed=9852679;
Sawai H., Ida A., Nakata Y., Koya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chondrodysplasia."
Hum. Mutat. 9:131-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97220591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS SMCD GLU-18 AND ARG-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lkegawa S., Nishimura G.,
FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE MINERALIZATION ZONES OF HYALINE CARTILAGE.

SUBUNIT: HOMOTRIMER.

SUBUNIT: HOMOTRIMER.

UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

DISEASE: DEFECTS IN COLIONI ARE THE CRUSE OF SCHMID TYPE METAPHYSEAL CHONDRODYSPLASIA (SMCD), A DOMINANTLY INHERITED DISCASE: DEFECTS IN COLIONI ARE THE CRUSE OF THE CARTURES OF THE PHENOTYPE ARE MILD SHORT STATURE, COXA VARA AND A WADDLING GRIT.

RADIOGRAPHY USUALLY SHOWS SCLEROSIS OF THE RIBS, ELARING OF THE RESULTANDERS OF THE CARTURES OF THE CARTURES OF THE CARTURES OF THE PHENOTYPE ARE MILD SHORT STATURE, COXA VARA AND A WADDLING OF THE PHENOTYPE ARE MILD SHORT STATURE, COXA VARA SHORD REALING OF THE CARTURES OF THE CARTURES OF THE CARTURES OF THE CARTURES OF THE PHENOTYPE ARE MILD SHORT STATURE, COXA VARA AND A WADDLING OF THE CARTURES OF THE PHENOTYPE ARE MILD SHORT STATURES.
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mura G., Nagai T., Hasegawa T., Ohashi H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLU-595; HIS-597; LYS-617;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Koyama K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maroteaux P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bateman J.F.;
ly in vitro is prevented
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the Schmid metaphyseal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as modified and this statement is not removed. U entities requires a license agreement (See htt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
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DISEASE: DEFECTS IN COL10A1 ARE THE CAUSE OF SPONDYLOMETAPHY DYSPLASIA (SMD). SMD COMPRISES A HETEROGENEOUS GROUP OF HERN SKELETAL DYSPLASIAS CHARACTERIZED BY MODIFICATIONS OF THE VERTEBRAL BODIES OF THE SPINE AND METAPHYSES OF THE TUBULAR -i- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
                                                                                                                                                                                                                                                                     CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 8.
                                                                                                                                                                                                                                                                                                                                                                                             MIM; 184250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute.
                                                                                                                                                                VARIANT
                                                                                                                                                                                     VARIANT
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                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                  Cartilage;
                                                                                                                                                                                                                                                                                                              Extracellular matrix;
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L; X65120; CAA6236.1; -.
L; X98568; CAA67178.1; -.
L; AL121963; CAB87590.1; -.
L; S68531; AAC60615.1; -.
L; X58879; CAA611686.1; -.
L; X58879; CAA61168.1; -.
L; X72579; CAA51170.1; -.
L; X72580; CAA51170.1; JOINEE
                                                                                                                                                                                                                                                                                                                                                                                                                                     S21856;
S26396;
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S30086;
A43901;
S18249;
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TB; PS01113; C1Q
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                                                                                                                        Similarity
                              GFPGSKGDPGSPGPPGPAGIATKGLNGPTGPPGPPGPRGHSGEPGLPGPPGPPGPPGQAV
                                                                      GNPGLPGPKGDPGVGGPPGLPGPVGPAGAKGMPGHNGBAGPRGAPGIPGTRGPIGPPGIP
                                                                                        GSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLP
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S18249.
S21856.
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S30086.
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                                                                                                                                                                                                                                                                                                              Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is copyright. It is produ
stitute of Bioinformatics
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                                                                                                              34;
                                                                                                                                                   /FTId=VAR_001840.
C -> R (IN SMCD).
/FTId=VAR_001841.
                                                                                                                      Score 418.5; DB 1
Pred. No. 3.5e-22;
                                                                                                                                                                                                                                                                                         Disease mutation; POTENTIAL.
                                                                                                                                                                                            /FTId=VAR_001838.
G -> R (IN SMCD)
/FTId=VAR_001839.
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                                                                                                                                                                                                                             -> E (IN SMCD)
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PRSAFSAKRSESRVPPPSDAPLPFDRVLVNE 132
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                                                                                                                                                                                                                                                  REGION
                                                                                                                                  DB 1;
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                                                                                                                                                                                                                                                                                                    Polymorphism.
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                                                                                                                                                                                                                                                                                                                                                                                                       "The cloning and sequencing of alpha 1(VIII) collagen cDNAs demonstrate that type VIII collagen is a short chain collagen and contains triple-helical and carboxyl-terminal non-triple-helical domains similar to those of type X collagen.";

J. Biol. Chem. 264:16022-16020/10001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1991
15-JUL-1999
                                                                                     EMBL;
                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Luvalle P., Ninomiya Y., Rosenblum N.D., Ols "The type Y collagen gene. Intron sequences region and separate the coding regions for terminal and triple-helical domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ninomiya Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken)
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                                                       PIR; A31896; A31896
                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89054019;
                                   InterPro; IPR001073; Clq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol.
                                                                                                                                                                                                                                                                   SIMILARITY: STRONG, TO SIMILARITY: CONTAINS 1
                                                                                                                                                                                                                                                                                    PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HOMOTRIMER.
                                                                                                                                                                                                                                                                                                                                                       3iol. Chem. 264:16022-16029(1989).
FUNCTION: TYPE X COLLAGEN IS PRODUCT OF HYPERTHROPHIC CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE MINERALIZATION ZONES OF HYALINE CARTILAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  developmentally regulated type X
reading frame without introns.";
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                                                                      M13496; AAA48736.1;
J04194; AAA48634.1;
   PF00386;
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                                                                                                                          requires a license agreement (S
an email to license@isb-sib.ch).
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   MEDLINE=96186528; PubMed=8606057; Petry F., McClive P.J., Botto M., Morl "The mouse Clq genes are clustered on conservation of gene organization."; Immunogenetics 43:370-376(1996).
-!- FUNCTION: C1Q ASSOCIATES WITH THB
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                                                                                                                                                               Eur. J. Biochem.
                                                                                                                                                                                precerebellin.";
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                                                                                                                                                                                                                                                                 STRAIN=ICR; TISSUE=Macrophage;
MEDLINE=93011118; PubMed=1396691;
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"Isolation, sequence analysis and characterization of cDNA clones coding for the C chain of mouse Clq. Sequence similarity of complement subcomponent Clq, collagen type VIII and type X and
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No. 4.4e-22;
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MGD; MGI:88225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R AND S IN THE MOLAR RATION OF 1:2:2. C1Q SUBCOMPONENT IS COMPOSED OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
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OF NINE SUBUNITS, SIX OF WHICH ARE
A AND B CHAINS, AND THREE OF WHICH
THE C CHAIN.
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                                                                                                       APGEKGEGGRPGLPGPRGDPGPRGEA---GPAGPTGPAGECSVPPR----SAFSAKRS
                                                                                                                                                      LLVLLLLGLAAGSPPLDDNKIPSLC---PGHPGLPGTPGHHGSQGLPGRDGRDGRPG
GESIASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGFL
                                                                                                                              LILLFLLAL----PL-RSQASAGCYGIPGMPGAPGKDGHDGLQGPKGEPGIPAVPG
                                                 ESRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKV
                                    TTQY-PEANALVRFNSVVTNPQGHYNPSTGKFTCEVPGLYYF
                                                                                   TQGPKGQKGEPGMPGHRGKNGPRGTSGLPGDPGPRGPPGEPGVEGRYKQKHQSVFTVTRQ
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f
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                                       VYYTSHTANLCVHLNLN
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Query Match
Best Local
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15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collagen genes.",
Biochem. J. 273:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thomas J.T., Kwan A.P.L., Grant M.E., Boot-Handford R.P.; "Isolation of cDNAs encoding the complete sequence of bovine type collagen. Evidence for the condensed nature of mammalian type {\tt X}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
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                                            DISULFID
MOD_RES
MOD_RES
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91113131; PubMed=1703407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL
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Pfam; PF01391; Collagen; 9.
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                                                                                                                                                                                                                                                                                                                                     entities requires
                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                  Cartilage;
                                                                                                                                                                                                       SMART:
                                                                                                                                                                                                                                                               InterPro;
InterPro;
                                                                                                                                                                                                                                                                                      PIR; S13301;
                                  SEQUENCE
                                                                                             DOMAIN
                                                                                                        DOMAIN
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                                                                                                                               DOMAIN
                                                                                                                                            CHAIN
                                                                                                                                                                               Extracellular matrix;
                                                                                                                                                                                         PROSITE; PS01113; C1Q;
                                                                                                                                                                                                                           PRINTS; PR00007; COMPLEMNTC10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chem. J. 273:141-148(1991).

TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE MINERALIZATION ZONES OF HYALINE CARTILAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMOTRIMER.
                                                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute.
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                                                                                                                                                                                                       SM00110; C1Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LARVASFCDHMFN-SKQVS-SGGALLRLQRGDEVW--LSVNDYNGMVGIEGSNSVFSGFL
                                                                                                                                                                                                                 PD000007; Collagen;
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                                                                                                                                                                                                                                                                          IPR001073; C1q.
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                                                                                                                                                                  Collagen;
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(Rel. 20, Last sequence up
(Rel. 38, Last annotation
pha 1(X) chain precursor.
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519
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                                     65546
                                                                                                                                                                                                                                                                Collagen.
                                                                                                                                                                  Signal;
                                                                                                                                                                  Connective tissue; Repeat; Hydroxylation; Signal; Glycoprotein.
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                                     Σ.
                                                                        NONHELICAL REGION (C1Q.
BY SIMILARITY.
HYDROXYLATION (BY S
   Score
Pred.
                                                                                                                    COLLAGEN ALPHA 1(X) CHAI NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION.
                                               HYDROXYLATION N-LINKED (GLC)
                                     CD4CA73A03E004CA
  411.5; DB 1;
No. 1.1e-21;
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(GLCNAC...) (POTENTIAL).
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE PROM N.A. Piddington C.S., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazpa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complement-clq tumor necrosis C1QTNF7 OR CTRP7.
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Submitted (J
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Pfam; PF01391; Collagen;
                                                                                                                                                                                                             EMBL; AF329839; AAK17963.1;
EMBL; BC022187; AAH22187.1;
Genew; HGNC:14342; C1QTNP7.
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SMART; SM00110; C1Q;
                                                                                                                                                                                        InterPro; IPR001073; Clq.
                 DOMAIN
                                                                                                PROSITE; PS01113; C1Q;
                                                                                                                                                                                [nterPro;
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and this statement is not removed
requires a license agreement (See
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                                                                                                                                                                                IPR000087; Collagen
                                                                                 Signal.
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38
141
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                                                  17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sheppard P.O., Bishop P., Lasser G.W.; mplement-clq tumor necrosis factor-related 000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                   COMPLEMNTC1Q.
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Primates;
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276
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289
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 POTENTIAL.

COMPLEMENT-C1Q TUMOR NECROSIS

RELATED PROTEIN 7:

COLLAGEN-LIKE. /

C1Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDA
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01-NOV-1995
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                                                                                                                                                                                                                                                                                                  STRAIN=129/Sv; TISSUE=Liver;
MEDLINE=93238750; PubMed=8477738;
Kong R.Y.C., Kwan K.M., Lau E.T.,
Grant M.B., Cheah K.S.B.;
                                                                                                                                                                                                                                                                                                                                                                                                    "The mouse collagen X gene: complete structure and expression pattern."; Biochem. J. 289:247-253(1993).
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Mammalia; Eutheria;
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                                                                                                                        MEDIINE=92267014; PubMed=1587271;
Apte S.S., Seldin M.F., Hayashi M., Olsen B.F.
"Cloning of the human and mouse type X collage
the mouse type X collagen gene to chromosome
Eur. J. Biochem. 206:217-224(1992).
                                                                                                                                                                                                                                                     "Intron-exon structure, alternative the mouse collagen X gene, Coll0a-1. Eur. J. Biochem. 213:99-111(1993).
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Elima K., Eerola I., Rosati R
de Crombrugghe B., Vuorio E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93143676; PubMed=8424763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BALB/c
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                                                         MEDLINE=92182017; PubMed=1543751;
                           Garofalo S.,
                                           Elima K.,
                                                                            STRAIN=C57BL/6;
                                                                                         SEQUENCE OF
                                                                                                                                                                                                          STRAIN=DBA/2J
                                                                                                                                                                                                                       SEQUENCE OF 51-680
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      Metsaeranta M., Kallio J., Pe
S., de Crombrugghe B., Vuorio
hybridization probes for mous
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Sciurognathi; Muridae; Murinae; Mus
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EMBL; X65121; CAA46237.1; -.
EMBL; X63013; CAA44741.1; -.
EMBL; Z21610; CAA79736.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This ESWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
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Biochim. Biophys.
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ProDom; PD000007; Collagen; 2.
SMART; SM00110; C1Q; 1.
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Pfam; PF01391; Collagen; 9.
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InterPro; IPR000087; Collagen.
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; S31216; S31216.
; S22215; S22215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTW: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS. SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIM. BIOPHYS. ACTA 1130:78-80(1992).
FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC CHONDROTOCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE MINERALIZATION ZONES OF HYALINE CARTILAGE.
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PSDAPL#FDRVI_VNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNG-ESIA 176
                                GIPGTRGPTGPPGVPGFPGSKGDPGNPGAPGPAGIATKGLNGPTGPPGPPGPRGHSGEPG
                                                                                             GLPGRDGRDGAPGAPGEKGEGGRPGLPGPR--
                                                                                                                                     GSPPLDDNKIPSLCPGHPGLP-----
                                                    --GPAGPTGPAGECSVP---
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COLLAGEN ALPHA 1(X) CHAIN.
NONHELICAL REGION (NC2).
TRIPLE-HELICAL REGION.
NONHELICAL REGION (NC1).
C1Q.
P -> L (IN REF. 3).
                                                                                                                                                         Score 408; DB 1; Pred. No. 1.9e-21;
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                                                                                                                                       -----GTPGHH-----GSQ 44
                                                                                                                                                                              Length 680;
                                                                                                                                                            Indels 88;
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                                                    PRSAFSAKRSESRVPP
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CQT2_HUMAN
ID CQT2_H
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Best Local S
Matches 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
-i- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
-i- SIMILARITY: CONTAINS 1 CLQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Piddington C.S., Bishop P.;

"Homo saplens complement-clq tumor necrosis factor-related protein.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00007; COMPLE SMART; SM00110; C1Q; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:14325; ClQTNF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Collagen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001073; Clq.
InterPro; IPR000087; Collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVGAPIPFDEILYNRQQHYDPRSGIFTCKIPGIYYFSYHVHVKGTHVWVGLYKNGTPTMY
                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS01113; C1Q;
KRSESRVPPPSDA---
                                                                    HDGDRGDSGEEGPPGRTGNRGKPGPKGKAGAIGRAGPRGPKGVNGTPGKHGTPGKKGPKG 130
                                                                                                               RDGAPGAPGEKGEGGRP----GLPGPRGDPGPRGEAGPAGP----TGPAGECSVPPRSAFSA
                                                                                                                                                              LLGAFARRDFRKGSPQL-
                                                                                                                                                                                           LLGLAA-----GSPPLDDNKIPSLC-----PGHPGLPGTPGHHGSQGLPGRDGRDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal.
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(Rel. 41, Last annotation updat
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143
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Primates;
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285
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285
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                                                                                                                                                                                                                                                      29;
                                                                                                                                                              ----VCSLPGPQGPPGPPGAPGPSGMMGRMGFPGKDGQDG
                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.

COMPLEMENT-C1Q TUMOR N

RELATED PROTEIN 2.

COLLAGEN-LIKE.
                                                                                                                                                                                                                                                                         Score 403;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                           C1Q.
; 7E31FF9868D4EDFA CRC64;
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Catarrhini; Hominidae;
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.8e-21;
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                            PLPFDRVLVNEQGHYDAVTGKFTCQ 146
    91;
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                                                                                                                                                                                                                                                                                                 Length 285;
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                                                                                                                                                                                                                                                           52;
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                                                                                                                                                                                                                                                           Gaps
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RESULT 11 CIQC_HUMAN
MEDLINE=91174759; PubMed=1706597; Sellar G.C., Blake D.J., Reid K.B.M.; "Characterization and organization of the genes encoding the A-, and C-chains of human complement subcomponent Clq. The complete derived amino acid sequence of human Clq.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugiyama T., Irie R., Utsuki i., was Kawakami B., Nagai K., Isogai T., Sugano S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIQG OR CIQC.
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21-JUL-1986 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C1QC_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complement Clq subcomponent,
                                                                                                                                                                                                                                                                                                           "Complete amino acid sequences of the present in subcomponent Clq of the
                                                                                                                                                                                                                                                                                                                                              Reid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hata H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Cerebellum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                 REVIEW OF C1Q DEFICIENCY MEDLINE=98450587; PubMed
                                                                                                                                                                                                                                                                                                                                                           MEDLINE=80020137;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 29-122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                     Immunobiology
                                                                                                                                                                                                                                                                                                                                                                                                                                         rissus=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQUENCE FROM N.A.
                                                                                                                                                                                                  Molecular basis of hereditary Clq deficiency.";
         NUMERICAL PROGRAMMENT OF THE SERVIC NAME CIR AND CIS TO YIELD FUNCTION: CIQ ASSOCIATES WITH THE PROENZYMES CIR AND CIS TO YIELD CI, THE FIRST COMPONENT OF THE SERVIM COMPLEMENT SYSTEM. THE COLLAGEN.LIKE REGIONS OF CIQ INTERACT WITH THE CA(2+)-DEPENDENT CIR(2)CIS(2) PROENZYME COMPLEX, AND EFFICIENT ACTIVATION OF CI TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF CIQ WITH THE FOR COMPLEXES.

FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES.

SUBUNIT: CI IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF CIQ, R AND S IN THE MOLAR RATION OF 1:2:2. CIQ SUBCOMPONENT IS COMPOSED OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE C CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE C CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191
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                                                                                                                                                                                                                                                                                                                                              K.B.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Nakagawa S., Senoh A., Mizuguchi H., Inaga
Nakagawa K., Mizuno S., Morinaga M., Kawamu
T., Irie R., Otsuki T., Sato H., Nishikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWPKPASLSGGAMVRLEPEDQVW
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O-LINKED GLYCANS CONSIST OF GLC-GAL DISACCHARIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakagawa S.,
                                                                                                                                                                                                                                                                                                                                                                                                           (MAY-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
Clq subcomponent, C chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 no acid sequence of 274:481-490(1991).
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                                                                                                                                                                                                                                     PubMed=9777412;
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                           the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        project.";
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mizuguchi H., Inagaki H., Suzuki Y.,
Morinaga M., Kawamura M.,
Sato H., Nishikawa T., Sugiyama A.,
                                                                                                                                                                                                                                                                                                               the three collagen-like regions first component of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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S

Matches

Conservative

33;

84;

Indels

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Gaps

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77
      Query Match
Best Local
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DOMAIN
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PIR; S14351;
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AK057792; BAB71575.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between
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Pfam; PF01391; Collagen; 1
                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 120575;
                                                                                                                                                                                                                                                                                                                                                                                                                   Genew;
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SMART; SM00110; C1Q; 1.
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InterPro; IPR000087; Collagen.
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INFECTIONS AND A HIGH PREVALENCE OF LUPUS I
SYMPTOMS. IT IS CHARACTERIZED BY A LOSS OF
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een the Swiss Institute of Bioinformatics
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3; Mismatches
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RT demonstrate that type VIII collagen is a short chain collagen and demonstrate that type VIII collagen is a short chain collagen and recontains triple-helical and carboxyl-terminal non-triple-helical recontains similar to those of type X collagen.";

RT domains similar to those of type X collagen.";

RI J. Biol. Chem. 264:16022-16029(1989).

CC -i. FUNCTION: MAJOR COMPONENT OF THE DESCEMET'S MEMBRANE (BASEMENT CC MEMBRANE) OF CORNEAL ENDOTHELIAL CELLS.

CC -i. SUBUNIT: MAJOR COMPONENT OF THE DESCEMET'S MEMBRANE (BASEMENT CC SUBUNIT: MAJOR COMPONENT OF THE THETROTRIMERS IN ASSOCIATION CC INTH ALPHA 2 (VIIII) TYPE COLLAGENS.

CC -i. SUBUNIT: MAY FORM HOMOTRIMERS, OR THE TRIPEPTIDE REPRATING COLLAGENS.

CC -i. MISCELLANEOUS: FOUR CONSECUTIVE GLY-PRO-PRO TRIPLETS ARE PRESENT CC INTER C-TERMINUS OF THE TRIPLE-HELICAL REGION. THESE MAY PROVIDE CLISTING AND THE TRIPLE-HELICAL REGION.

CC -i. SIMILARITY: STRONG, TO ALPHA 2 TYPES VIII AND X COLLAGENS.
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01-JAN-1990 (Rel. 13, Last sequence up
01-NOV-1995 (Rel. 32, Last annotation
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Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long a modified and this statement is not removed.
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   PROSITE; PS01113; CIQ; 1.

Extracellular matrix; Connective tissue; Repeat; Glycoprotein; Cell adhesion; Collagen; Signal. SIGNAL 1 20
                                                                                                                                                                                                                                                                                                                                                    EMBL; J05042; AAA31204.1; -.
                                                                                                                          PRINTS; PR00007; COMPLEMNTC1Q.
SMART; SM00110; C1Q; 1.
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Pfam; PF01391; Collagen; 8.
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InterPro; IPR000087; Collagen.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=95167486; PubMed=7863331;
Davis J.G., Oberholtzer J.C., Burns F.R., Greene M.I
"Molecular cloning and characterization of an inner
"Molecular cloning and characterization of an inner
                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Inner ear-specific collagen precursor (Saccular collagen).
Lepomis macrochirus (Bluegill).
Lepomis macrochirus (Bluegill).
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
Centrarchide; Lepomis.
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01-NOV-1995 (Re
                                                                                                                                                                               CIDSON 1.;
Submitted (MAR-1995) to the SWISS-PROT data bank.
-i- FUNCTION: FORMS A MICROSTRUCTURAL MATRIX WITHIN THE MEMBRANE (PROBABLY).
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                                                                                                                                                                                                                                                          Science 267:1031-1034(1995).
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                                                                                                                                                                                                                     Gibson T
                                                                                                                                                                                                                                 CONCEPTUAL TRANSLATION.
                                                                                                                                        TISSUE SPECIFICITY: SPECIALIZED SECRETORY SUPPORTING OUTER PERIMETER OF THE SACCULAR EPITHELIUM. SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                 CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT HAD TO BE INTRODUCED FOR POSITIONS 391-419 SO AS TO MAXIMIZE THE SIMILARITY
                                                                                                    WITH OTHER SHORT-CHAIN COLLAGENS.
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                                                              ROT entry is copyright. It is produced through Swiss Institute of Bioinformatics and the EV
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                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=91231001; PubMed=2029894;
MURAGAKI Y., Mattei M.-G., Yamaguchi N., Olsen B.R.,
Muragaki Y., Mattei M.-G., Yamaguchi N., Olsen B.R.,
"The complete primary structure of the human alpha 1
assignment of its gene (COL8A1) to chromosome 3.";
assignment of its gene (COL8A1) to chromosome 3.";
assignment of its gene (COL8A1) to chromosome 3.";
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P27658; Q96D07;
01-AUG-1992 (Rel
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15-JUN-2002 (Rel. 41, I
15-JUN-2002 (Rel. 41, I
Collagen alpha 1(VIII)
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Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: MAJOR COMPONENT OF THE DESCENET'S MEMBRANE
MEMBRANE) OF CORNEAL ENDOTHELLAL CELLS.
-i- SUBUNIT: MAY FORM HOMOTRIMERS, OR HETEROTRIMERS IN P.
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606
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Mammalia; Eutheria;
                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                              COVPGVYYFAVHATVYRASLQFDLVKNGESIA-SFFQFFGGWPKPASLSGGAMVRLBPED
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                                                                                                                                                                                                                                                                                            PGVAGLHGPPGKPGALGPQGQPGLPGPPGPPGPPGPPAVMPPTPPPQGEYLPDMGLGIDG
                                  RVFLQMPSEQAAGLYAGQYVHSSFSGYLLY
                                                                         OVWVQVGVGDYIGIYASIKTDSTFSGFLVY
                                                                                                                    CEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYDEYKKGFLDQA-
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PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REFERENCE (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

MISCELANBOUS: FOUR CONSECUTIVE GLY-PRO-PRO TRIPLETS ARE PLAIT THE C-TERMINUS OF THE TRIPLE-HELICAL REGION. THESE MAY THE HIGH THERMAL STABILITY OF THIS REGION.

THE HIGH THERMAL STABILITY OF THIS REGION. non-profit institutions as long and this statement is not removed requires a license agreement (See S15435 COL8A1. Bioinformatics It is produced through (See http://www.isb-sib.ch/announce/ There are no rest Usage and the restrictions DE REPEATING CHAINS. and EMBL outstation 18 ģ for collaboration L outstation -PRESENT 'n commercial 2 2

ProDom; PD000007; Collagen; SMART; SM00110; C1Q; 1. PROSITE; PS01113; C1Q; 1. MIM; 120251; Glycoprotein; SIGNAL Extracellular InterPro; IPR001073; C1q. InterPro; IPR000087; Coll Similarity 744 118 572 609 262 297 297 344 382 388 454 464 Conservative adhesion; 344 382 388 454 464 601 631 73364 MW; 27.8%; Collagen. Connective 34; Score Pred. P -> Collagen; Þ NONHELICAL C1Q. COLLAGEN ALPHA 1 (VIII)
NONHELICAL REGION (NC2)
TRIPLE-HELICAL REGION (NC1) 2BC1B0955DE2C9A3 Mismatches tissue; 4 8 8 8 E លក្ន 368; No. 1 ίΩ Signal. REF. DB 1; .2e-18; Repeat; Hydroxylation; 84; Length CRC64; Indels (COL1) 62; Gaps

GPRGDPGPRGEAGPAGPTGP---

AGECS

74

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PPSDAPLPFDRVLVNEQGHYDAVTGKFT

203 654 144 594 99

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01-NOV-1995 (Ref. 32,
15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA18_MOUSE
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Mus musculus (Mouse).
Bukanyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Alpha 1(VIII)-collagen gene transcripts encode a short-chain collagen polypeptide and are expressed by various epithelial, endothelial and mesenchymal cells in newborn mouse tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92362626; PubMed=1499564; Muragaki Y., Shiota C., Inoue M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
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-i- FUNCTION: MAJOR COMPONENT OF THE DESCEMET'S MEMBRANE MEMBRANE) OF CORNEAL ENDOTHELIAL CELLS.
                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There are the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki
                          EMBL; AK018742; BAB31383.1; PIR; S23779; S23779.
                                                                                         EMBL; X66976; CAA47387.1; -.
                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             łayashizaki Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: MAY FORM HOMOTRIMERS, OR HETEROTRIMER WITH ALDHA 2(VIII) TYPE COLLAGENS.
TISSUE SPECIFICITY: HIGH LEVELS IN CALVARIUM, NEWBORN MICE; ALSO IN VARIOUS EPITHELIAL, ENDOMESENCHYMAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: STRONG, TO ALPHA 2 TYPE SIMILARITY: CONTAINS 1 C1Q DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS. SIMILARITY: STRONG, TO ALPHA 2 TYPES VIII AND X COLLAGENS.
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Pfam; PF01391; Collagen;
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SIGNAL
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InterPro; IPR000087; Collagen.
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                                            GIFTCEVPGVYYFAYHVHCKGGNVWVALFKNNEPMMYTYDEYKKGFLDQA-
                                                                                             GIDGVKTPHAYAGKKGKHGGPAYEMPAFTAELTVPFPPVGAPVKFDKLLYNGRQNYNPQT
                                                                                                                                                                                        PGLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIVGPSGPIPGPKGEPGLPGPPGF
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                                                                   GKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIA-SFFQFFGGWPKPASLSGGAMVRL 199
RPGDQVFLQMPSEQAAGLYAGQYVHSSFSGYLLY
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H -> Y (IN REF. 1).
K -> KG (IN REF. 2).
P -> L (IN REF. 1).
P -> A (IN REF. 2).
IP -> SR (IN REF. 1).
D -> H (IN REF. 1).
T -> P (IN REF. 2).
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MPS -> NFF (IN REF. 2).
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Pred. No. 1.5e
36; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                 NONHELICAL REGION (NC1).
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Search completed: June 20, Job time : 38 secs 2003, 11:25:04

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16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.4	16.5	16.6	16.6	16.6	16.6	16.6	16.6	16.7	16.7	16.8	16.8	16.8	16.8	17.0	17.7	17.7	17.9	18.0	18.0	18.0	18.2
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Q62032	Q9YIB4	Q62033	Q62031	Q28396	093419	Q14046	017038	Q8R1P2	063079	Q99LL6	Q94399	Q8R066	Q9D0W2	Q20142	Q9TT06	077782	097405	806160	001945	Q9QXP7	017036	062789	Q99K41	077087	Q9Y6C2	Q9UG76	Q96G58	0961Н6
Q62032 mus musculu	cym		mus	æ	093419 gallus gall	Q14046 nomo sapien		\sim		Q99116 mus muscutu	Q94399 caenorhabdi	- 01	Q9d0w2 mus musculu	Q20142 caenorhabdi		077782 oryccolagus	097405 haliotis di	Q919q8 brachydanio	001945 meloldogyne	Q9qxp7 mus musculu	017036 caenornabdi		Q99K41 mus musculu	077087 alvineria p	Q9y6C2 nomo sapien	omo	nomo	homo

ALIGNMENTS

Q	οъ	Ş	문	Q	Query Ma Best Loo Matches		DR E			2 Z				36					DT O	ij	RESULT 1
121 APLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQ 180 	61 APGEKGEGGRPGLPGPRGEAGPRGAAGPMGAIGPAGECSVPPRSAFSAKRSESRVPPPAD 120	61 APGEKGEGGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSD 120	1 MRPLIALLLIGIVSGSPPLDDNKIPSLCPGQPGLPGTPGHHGSQGLPGRDGRDGRDGAPG 60	1 MRPLLVLLLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPG 60	Query Match 94.6%; Score 1254; DB 11; Length 243; Best Local Similarity 93.4%; Pred. No. 5.1e-100; Matches 227; Conservative 7; Mismatches 9; Indels 0; Gaps 0;	Hypothetical protein. SEQUENCE 243 AA; 25420 MW; 498129CD051DB97B CRC64;	EMBL; BC025174; AAH25174.1;	Submitted (MAR-2002) to the EMBL/GenBank/DUBU databases.	SEQUENCE FROM N.A.	Submitted (FRB-2002) to the EMBL/GenBank/DDBJ databases.	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=10090;	Mammalia: Rutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.	mus musculus (mouse). Turariota, Morazoa, Chordata, Craniata, Vertebrata, Euteleostomi;	Similar to DKFZP58680621 protein (Hypothetical 25.4 KDa protein).	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)	(TrEMBLrel. 21, Last	O1-JUN-2002 (TrEMBLrel. 21, Created)	Q8R002 PRELIMINARY; PRT; 243 AA.	.

2919Qs

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RESULT

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Q95JD7
ID Q95J
AC Q95J
DT 01-D
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Best Local Simi
Matches 100;
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Q95MQ4;
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Eukaryota; Metazoa; Chordata; Craniat
Mammalia; Eutheria; Cetartiodactyla;
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MEDLINB=21369933; PubMed=11382781;

MEDLINB=21369933; PubMed=11382781;

Sato C., Yasukawa Z., Honda N., Matsuda T., Kitajima K.;

Sato C., Yasukawa Z., Honda N., Matsuda T., Kitajima K.;

Tidentification and Adipocyte Differentiation-dependent Expressible Unique Disialic Acid Residue in an Adipose Tissue-specific the Unique Disialic Acid Residue in an Adipose Tissue-specific
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01-DEC-2001 (TREMBLrel. 19, Last sequence up
01-UN-2002 (TREMBLrel. 21, Last annotation
adipose tissue-specific protein adipo Q.
 Q95JD7
Q95JD7;
Q1-DEC-2001
01-DEC-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein, Adipo Q.";
J. Biol. Chem. 276:28849-28856(2001).
EMBL; AF269230; AAK58902.1; -.
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InterPro; IPR000087; Collagen.
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                                                                                                                                                                                                                                                                                                                                                                                 GEKGEKGDAGILGPKGETGDVGMTGAEGPRGFPGTPGRKGEPGEAAYVYRSAFSV-GLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLLLLALPSHGEDNMEDPPLPKGACAGWMAGIPGHPGHNGT---PGRDGRD-----GTP
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(TrEMBLrel. 19, (TrEMBLrel. 19, TrEMBLrel. 21,
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                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.1%;
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Pred. No. 7.1
   Created)
Last sequence update)
Last annotation updat
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actyla; Ruminantia; Pecora; Bovoidea
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Q9N178
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Best Local Simi
Matches 104;
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EMBL; AF404407; AAK92202.1; -.
InterPro; IPR001073; C1q.
InterPro; IPR001087; Collagen.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 1.
ProDom; PD000007; Collagen; 1.
PROSITE; PS01113; C10; UNKNOWN 1
SEQUENCE 243 AA; 26264 MW; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macaca mulatta (Rhesus macaque).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adiponectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hotta K., Funahashi T.,
Hansen B.C., Matsuzawa )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=ADIPOSE TISSUE;
MEDLINE=21232234; PubMed=11334417;
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                                                                                                                                                                                                                                                                                                                                           Q9N178;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        progression to type 2 diabetes
                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                SBQUENCE FROM N.A.

MEDLINE=21015405; PubMed=11130976;

Nielsen V.H., Bendixen C., Arnbjerg

Shukri N.M., Thomsen B.;
                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                    Type X collagen.
           in type X collagen.";
Mamm. Genome 11:1087-1092(2000).
EMBL; AF222861; AAF37271.1; -.
                                                                                                                                                                        NCBI_TaxID=9823;
                                                                                                                                                                                                                                   Sus scrofa (Pig).
                                                                    'Abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKAMLFTYDQYQENNVDQA -- SGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTFTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPGEKGEKGDPGLIGPKGDTGETGVTGAEGPRGFPGIQGRKGEPGEGAYVYRSAFSV-GL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLLYHD
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                                                                    growth plate
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                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
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15,
21,
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                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation updat
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Pred. No. 1.4e-28;
                                                                                                                                                                                                                                                                                                                             Created)
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243;

26;

Gaps

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229

Euteleostomi; Sus.

Jensen H.B.,

InterPro; IPR001073; C1q. InterPro; IPR000087; Collagen

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ID 1Q9
ID 2Q9
ID 7Q9
ID 7Q9
ID 701
ID
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Matches 99
Best Loc
Matches
                     Query Match
Best Local
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Pfam; PF01391; Collagen; 8.
PRINTS; PR000007; COMPLEMNTC1Q.
ProDom; PD000007; Collagen; 2.
SMART; SM00110; ClQ; 1.
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Q9Z1K4;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Collagen alpha 1 type X (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat)
                                                                                                                  PRINTS; PROGOO7; COMPLEMANT
SMART; SMOOILO; CIQ; 1.
PROSITE; PSOILL3; CIQ; 1.
                                                                                                                                                                                                                                                                                                                                                     Marks S.A., Lundmark C., Christersson C., Wurtz T., Odgren P.R. Seifert M.F., MacKay C.A., Mason-Savas A., Popoff S.E.; "Endochondral bone formation in toothless (osteopetrotic) rats:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                           PROSITE;
                                                                                                                                                                                                  Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20310874; PubMed=10853827;
                                                                                                                                                                                                                                                                                        EMBL; AJ131848; CAA10518.1; -.
                                                                                                                                                                                                                                                                                                              failures of chondrocyte patterning a Int. J. Dev. Biol. 44:309-316(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                 InterPro;
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94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIA-SFFQFFGGWPKPASLSGGAMVR 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPPEGFVKEGQRAFVSANQGVTGMPVSAFTVILSKAYPAIGAPIPFDKILYNGQQHYDPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGIFTCRIPGIYYFSYHIHVKGTHAWVGLYKNGTFVMYTYDBYVKGYLDQA--SGSAILD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    675 AA; 65447 MW;
                                                                                                                                                                                                                                              IPR001073; Clq.
IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                        295 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
    Conservative
                                                                                                                                                                               COMPLEMNTC1Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.4%;
                                                                                      30012 MW;
                       30.3%;
36.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 415.5;
Pred. No. 1.
                       Score 402;
Pred. No. 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26397B10310383F9
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                                                                                        FF43B1548028813E
    Mismatches
                                                                                                                                                                                                                                                                                                                                       and type X collagen expression.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GPRGDPGPRGEA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .7e-27;
                       DB 11;
3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               672
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                                                                                             CRC64;
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                                            Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                         P.R.,
       52;
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         Gaps
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RESULT 6
Q9D8U4
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            Query Match
Best Local 9
 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9D8U4
                                                             PRINTS; PRO0007; COMPLEMNICIA.
SMART; SM00110; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                        EMBL; AK007683; BAB25187.1; -. MGD; MGI:1916433; 1810033K05Rik.
                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1810033K05RIK
                                                                                                                                                                      InterPro; IPR001073;
InterPro; IPR000087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L810033K05Rik
                                                                                                                                    Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 2.
                                                                                                                                                                                                                                                                             Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSLCPGH-----PGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGB------KGB
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                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTGMPVSAPTVILSKAY--PAVGAPIPPDEILYNRQQHYDPRSGIFTCKIPGIYYPSYHI
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=PANCREAS
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GDPGPRGEAGPAGPTGPAGECSVP---
                                                                                                                                                                      Collagen
 29.8%; Score 395; DB 11; 35.9%; Pred. No. 3.7e-26; tive 31; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Buteleosto
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                    6D3905AE7C19E6FA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294
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                                                                        CRC64;
                                  Length 294;
       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
       44;
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       Gaps
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RESULT 7
Q95J95
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Best Local Similarity
Matches 90; Conserv
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01-DEC-2001
01-JUN-2002
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Regulation of Adiponectin gene expression in Submitted (SEP-2001) to the EMBL/GenBank/DDBJ EMBL; AP417206; AAL09702.1; -. InterPro; IPR001073; C1q. InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q95J95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kabir M., Ananthnarayan S.,
Dea M.K., Bergman R.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=ADIPOSE TISSUE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q95J95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PP00386; Clq; 1.
Pfam; PP00391; Collagen; 1.
ProDom; PD0000007; Collagen; 1.
PROSITE; PS01113; ClQ; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGI-YASIKTDSTFSGFLVYSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPCSCGSSRAKSAFSVAVTKSYPRERLPIKFDKILMNEGGHYNASSGKFVCSVPGIYYFT
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                                                                                                                                                                                                                                                                                                       LLLGLAAGSPPLDDNKIPSLCPG-HPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKG
                                                                                                                  PSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIAS
                                                                                                                                                                                   EKGDPGLVGPKGDTGETGVTGVEGPRGFPGTPGRKGEPGESAYVHRSAPSV-GLESRITV
                                                                                                                                                                                                                                                                                 VLLPLPKGA-----
                                                                                         P-NVPIRFTKIFYNLQNHYDGTTGKFHCNIFGLYYFSYHITVYLKDVKVSLYKKDK--AM
                                                                                                                                                                                                                                    EGGRPGLPGPRGD--
LFTYDQYQEKNVDQASGSVLLHLEVGDQVWLQV
                                            FFQFFGGWPKPA-SLSGGAMVRLEPEDQVWVQV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194
194 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                 28.2%;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                           Score 373.5; DB 6
Pred. No. 1.6e-24;
2; Mismatches 66
                                                                                                                                                                                                                                  --PGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPP
                                                                                                                                                                                                                                                                                      CPGWMAGI PGHPGHNGT ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PQGPPGPPGAPGSSGVVGRMGFPGKDGQDGQDGDRGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3AA3D947D187AF9A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kim S.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6;
                                                                                                                                                                                                                                                                                                                                                                             66;
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RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kubhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kubhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilning L.,
RA Havashizaki V.
RA Havashizaki V.
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Best Local
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Q9D2V4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRODOOT; COMPLEMENT.

PRINTS; SMOO110; C10; 1.

SMART; SMOO1113; C10; 1.

PROSITE; PSO1113; C10; 1.

PROSITE; PSO1113; C10; 1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 7.
PRINTS; PR00007; COMPLEMNTCLQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001).
EMBL; AK018742; BAB31383.1;
MGD; MGI:88463; Col8a1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001073; Clq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                layashizaki Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                œ
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                                                                                                                                                                                               965
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                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                           536
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            714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                       VPGLLGPKGEPGIPGDQGLQGPPGIPGIVGPSGPIGPPGIPGPKGEPGLPGPPGPPGVGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shinagawa A., Shibata K.,
                                                                                                                                                                                                                                                                                        PGVAGLHGPPGKPGALGPQGQPGLPGPPGPPGPPGPPAVMPTPSPQGEYLPDMGLGIDGV
                                                                                                                                                                                                                                                                                                                                                                                                                            IPSLC--PGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLP-----
            VFLOMPSEQAAGLYAGQYVHSSFSGYLLY 742
                                                                                                     EVPGVYYFAYHVHCKGGNVWVALFKNNEPMMYTYDEYKKGFLDQA--SGSAVLLLRPGDQ
                                                                                                                                           QVPGVYYFAVHATVYRASLQFDLVKNGESIA-SFFQFFGGWPKPASLSGGAMVRLEPEDQ
                                                                                                                                                                                                                                                 PPRSAFSAKR----
                                                                                                                                                                                                 KPPHAYAGKKGKHGGPAYEMPAFTAELTVPFPPVGAPVKFDKLLYNGRQNYNPQTGIFTC
                                                         VWVQVGVGDYIGIYASIKTDSTFSGFLVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type VIII,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.0%; Score 370.5; 34.6%; Pred. No. 1.40 tive 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17, Last sequence up 17, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha 1.
                                                                                                                                                                                                                                                                                                                                        GPRGDPGPRGEAGPAGPTGP--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C659BDCCBCD6EB9C CRC64;
                                                                                                                                                                                                                                            --SESRVP-PPSDAPLPFDRVLVNEQGHYDAVTGKFTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yoshino M.,
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                Query Match
Best Local S
Matches 93
Strausberg R.;
Submitted (SEP-2001) to the EMBL,
Submitted (SEP-2001) To the EMBL,
EMBL; BC013581; AAH13581.1; -.
EMBL; BC013581; AAH13581.1; -.
InterPro; IPR0001073; Clq.
InterPro; IPR000087; Collagen.
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01-DEC-2001 (
01-DEC-2001 (
01-JUN-2002 (
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01-DEC-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
Procollagen, type VIII,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; F
Collagen.
SEQUENCE
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Q96D07;
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pfam; PF01391; Collagen; 7.
prOSITE; PS01113; C1Q; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001073; C1q.
InterPro; IPR000087; Collagen.
                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                      Hypothetical
                                                                                                                                                                                                          NCBI_TaxID=9606/
                                                                                                                                                    TISSUE=LUNG;
                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGVAGLHGPPGKPGALGPQGPGLPGPPGPPGPPGPPAVMPTPSPQGEYLPDMGLGIDGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VWVQVGVGDYIGIYASIKTDSTFSGFLVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   744 ÁA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                               (TIEMBLrel. 19, Created)
(TIEMBLrel. 19, Last sequence update)
(TIEMBLrel. 21, Last annotation update)
1 73.4 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.0%; Score 370.5; DB 11; Length 744; 34.6%; Pred. No. 1.4e-23; 1ve 32; Mismatches 83; Indels 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 19, Created)
. 19, Last sequence upo
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, alpha 1.
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                           Craniata; Vertebrata;
Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                        Buteleostomi;
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Best Local
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pROSITE; PS01113; CIQ; UNKNOWN.
Collagen; Hypothetical protein.
SEQUENCE 744 AA; 73364 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01391; Collagen; 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata;
Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
FLJ00201 protein (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLJ00201 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     iomo sapiens (Human)
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                                                                                                                                                                                                                                           GLQGPAGPIGPQGLPGL-KGEPGLPGPPG-EGRAGEPGTAGPTGPPGVPGSPGITGPPGP
                                                                                                                                                         PGLPGPRGDPGPRGEAGPAG---PTGPA---
G-BSIASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFSGF
                                                                                                      SRVP-PPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKN
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                                                                                                                                                                                                                                                                                                                                                                                                                    705 AA; 67430 MW;
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                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                    - PPPASGMPVKFDRTLYNGHSGYNPATGIFTCPVGGVYYFAYHVHVKGTNVWVALYKN
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73364 MW; 2BC1B0955DE2C9A3
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                                                                                                                                                                                                                                                                                                                                27.4%; Score 363.5;
39.3%; Pred. No. 5.26
tive 25; Mismatches
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Catarrhini; Hominidae;
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.2e-23;
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Hominidae; Homo.
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ne isolated
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Complement component 1, q subcomponent, alpha polypicion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUB=KIDNEY:
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:88223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                             SMART;
                                                                                                                                                                                                                                                                                                                                           PRINTS;
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InterPro; IPR000087; Coll
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                                                                                                                                                                                                                                                                                                      ; PR00007; COMPLEMN
SM00110; C1Q; 1.
E; PS01113; C1Q; 1.
                                                                                                                                                                                                          79;
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                                               SGPQGLKGVKGNPGNIRDQPRPAFSAIRQN---PMTLGNVVIFDKVLTNQESPYQNHTGR
                                                                                                                             PGNPGRPGLKGERGEPGAAGI -- RTGIRGFKGDPGESGPPGKPGNVGLPGPSGPLGD
                                                                                                                                                                PGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAPGEKGEGGRPGLPGPRGDPGPRGEAGP
            FTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWPKPA--
                                                                                       AGPTGPAGECSVP----
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                                                                                                                                                                                                                                                                                       245 AA;
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                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; BAB22262.1;
; AAH02086.1;
; Clqa.
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                                                                                                                                                                                                                                                                                       25974 MW; 41C2066D49592020 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      Collagen
                                                                                                                                                                                                                             23.7%;
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                                                                           -PRSAFSAKRSESRVPPPSDAPLPFDRVLVNEQGHYDAVTGK
                                                                                                                                                                                                        Score 314; DB 11;
Pred. No. 2.7e-19;
'4; Mismatches 85;
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Q9ES30;
01-MAR-2001
01-MAR-2001
01-DEC-2001
                           Q920N0;
01-DEC-2001
01-DEC-2001
01-JUN-2002
HP-20.
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                                             (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 21,
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Pfam; PFULSON, COMPLEX-PRINTS; PRO0007; COMPLEX-SMART; SMO0110; C1Q; 1.
SMART; SP001113; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
PROSITE; PS01113; C1Q; 1.
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SEQUENCE FROM N.A.
MEDLINE=21264842; PubMed=11071891;
MARGHAT., Abe M., Kurisu K., Jikko A., Furukawa S.;
MAGGAT., Abe M., Kurisu K., Jikko A., Furukawa S.;
"Molecular cloning and characterization of a novel (
"Molecular contactive secretory protein and its possi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001073; Clq.
InterPro; IPR0000087; Collagen.
Pfam; PF00386; Clq; 1.
Pfam; PF01391; Collagen; 1.
PRINTS; PR00007; COMPLEMNTC1Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoding a putative secretory protein
skeletal development.";
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MGD; MGI:1932136; Cors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 276:3628-3634(2001).
IBL; AF246265; AAG33704.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLPLLFLPFCLCQDEYMESPQAGGLPPDCSKCCHGDYGFRGYQGPPGPPGPPGPPGIPGNHGN
                                                                                                                                                                                                                                                                                  VKNGESIASFFQFFGGWPKPASLSGGAMVRLEPEDQVWVQVGVGDYIGIYASIKTDSTFS
                                                                                                                                                                                                                                                                                                                                   ATHFSNONSGIIFSSVETNIGNFFDVMTGRFGAPVSGVYFFTFSMMKHEDVBEVYVY--L
                                                                                                                                                                                                                                                                                                                                                                          SRVPPPSDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAV----HATVYRASLQFDL
                                                                                                                                                                                                                                                                                                                                                                                                                NGNNGATGHEGAKGE-----KGDKGDLGPRGERGQHGPKGEKGYPGVPPELQIAFMASL
                                                                                                                                                                                                                  GPLVY 233
                                                                                                                                                                                                                                                       MHNGNTVFSMYSYBTKGKSDTS-SNHAVLKLAKGDEVWLRMGNG---ALHGDHQRFSTFA
                                                                                                                                                                            GFLLF 243
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                                                                          PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .20.4%; Score 270.5; DB 1
31.8%; Pred. No. 1.5e-15;
tive 33; Mismatches 107
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Last sequence update)
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Sciurognathi; Muridae; Murinae; Mus
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possible involvement in
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RESULT 15
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InterPro; IPR001073; C1q.
InterPro; IPR001097; Collagen.
Pfam; PP00386; C1q; 1.
Pfam; PP01391; Collagen; 1.
PROSITE; PS01113; C1Q; UNKNOWN 1.
SEQUENCE 196 AA; 21330 MW; B071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tamias sibiricus (Siberian chipmunk) (Asian chipmunk).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21488336; PubMed=11602349;
Ono M., Hosoe Y., Azuma S., Shoji M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=64680;
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Q919Q7;
01-OCT-2000
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                                                                                                                                                                                                                                           Carassius auratus (Goldfish).
Bukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cyprinidae; Carassius.
                                                                                                                                                                                                                                                                                                                   01-OCT 2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21, Mannose binding-like lectin
                                                                                                             MEDIINE-20456722; PubMed=11003389; WILLINE-20456722; PubMed=11003389; Vitved L., Holmskov U., Koch C., Teisner B., Hansen S., Skjodt Vitved L., Holmskov U., Koch C., Teisner B., Hansen S., Skjodt The homologue of mannose-binding lectin in the carp family C. "The homologue of mannose-binding lectin in the deduced primary is expressed at high level in spleen, and the deduced primary is expressed at fight level in spleen, and the deduced primary structure predicts affinity for galactose.";
                                                                                                                                                                                                                                                                                                      MBL.
                                                                  Immunogenetics 51:955-964(2000).
EMBL; AF227739; AAF63470.1; -.
HSSP; P35247; 1808.
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                             NCBI_TaxID=7957;
InterPro; IPR001304; Lectin_C.
Pfam; PP01391; Collagen; 2.
Pfam; PP00059; lectin_C; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                       TISSUE=LIVER;
                                                         InterPro; IPR000087; Collagen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPSE-PVVFTEVLYNTORDLKASTGVFNCVBPGNYHFSFDVBLYHCKVKIGLMKNHIOVM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCFLISS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 266.5; DB 11;
Pred. No. 2.5e-15;
Pred. No. 2.5e-15;
                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nara K.,
                                                                                                                                                                                                                                                                                                                                                                                                  246
                                                                                                                                                                                                                                                                  Vertebrata; Euteleostomi;
Ostariophysi; Cypriniformes;
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                                                                                                                                                   family Cyprinidae
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Search completed: June 20, Job time : 63 secs

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PROSITE;
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VARIANT
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195
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                                                                                                                                                                                                                                                                      Signal.
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                                                                                                                                 EKGEG-----GRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPP
                                                                                                                EKGESGVSVQGPPGKAGPPGTAGEKGERGPSGPQGSPGSESVLESLKSEIQQLKAKI---
                                                                                                                                                     SDAPLPFDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQPDLVKNGESIASF 178
                  --SGFLVYSDW 236
                                                      FQFFGGWPKPASLSGGAMV--RLEPEDQVWVQV----GVGD---YIGIYASIKTDSTF--
                                                                           ----ATFEK--VSSVCHFRKV----
 TECKQLIFINW
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C_TYPE_LECTIN_2; 1.
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                                                                                                                                                                                                                                           POTENTIAL.
S -> F.
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Pred. No. 5.2e-14;
3; Mismatches 73;
                                                                                                                                                                                                                                    AB692282D289D0D5 CRC64;
                                                                              -GQKYYITDGVVG----NFD-----QGLKSC 146
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